

GTTTAGTCTGCAGCCGAGCAGCTAAAGGGAGAAAGAAATCGCTCAGGAAAGACACACTGCAGACTCCACCGGCACCCCTGC	79
AATAGATGGTTCGACTACACAAGGGAGAAAACGGGAGGTGACACTCTCTGCCCTGGAAAAGAGGACGAAACGACCAAA	158
CAAACGCAAGGACTGGACTCCATGCCGAAGGTATCTGGAAGTCGTGACACCGGTGTGTATATAAAACAAAAGTTTGGAGCT	237
GTTAATTGCTGTGCTGTGTTATTAAAGAGACGCTTTCAAGTTTCAAGTACCAAAATGTAGCTTTACGTTGCCAAAGGAAGT	316
TGAGGCAATTGCTTGTCTGTTTAACTTGCTCTGTGAGGAAATCTCATAAACTGACCA ATG CAC CAA ATG AAT	5 390
A K M H F R F V F A L L I V S F N H D V	25
GCT AAA ATG CAC TTT AGG TTT GTT TTT GCA CTT CTG ATA GTA TCT TTC AAC CAC GAT GTA	450
L G K N L K Y R I Y E E Q R V G S V I A	45 510
CTG GGC AAG AAT TTG AAA TAC AGG ATT TAT TAT GAG GAA CAG AGG GTT GGA TCA GTA ATT GCA	510
R L S E D V A D V L L K L P N P S T V R	65
AGA CTA TCA GAG GAT GTG GCT GAT GTT TTA TTG AAG CTT CCT AAT CCT TCT ACT GTT CGA	570
F R A M Q R G N S P L L L V V N E D N G E	85
TTT CGA GCC ATG CAG AGG GGA AAT TCT CCT CTA CTT GTA GTA AAC GAG GAT AAT GGG GAA	630

1/361

Fig. 1A

I S I G A T I D R E Q L C Q K N L N C S	105
ATC AGC ATA GGG GCT ACA ATT GAC CGT GAA CAA CTG TGC CAG AAA AAC TTG AAC TGT TCC	690
I E F D V I T L P T E H L Q L F H I E V	125
ATA GAG TTT GAT GTG ATC ACT CTA CCC ACA GAG CAT CTG CAG CTT TTC CAT ATT GAA GTT	750
E V L D I N D N S P Q F S R S L I P I E	145
GAA GTG CTG GAT ATT AAT GAC AAT TCT CCC CAG TTT TCA AGA TCT CTC ATA CCT ATT GAG	810
I S E S A A V G T R I P L D S A F D P D	165
ATA TCT GAG AGT GCA GCA GTT GGG ACT CGC ATT CCC CTG GAC AGT GCA TTT GAT CCA GAT	870
V G E N S L H T Y S L S A N D F F N I E	185
GTT GGG GAA AAT TCC CTC CAC ACA TAC TCG CTC TCT GCC AAT GAT TTT TTT AAT ATC GAG	930
V R T R T D G A K Y A E L I V R E L D	205
GTT CGG ACC AGG ACT GAT GGA GCC AAG TAT GCA GAA CTC ATA GTG GTC AGA GAG TTA GAT	990
R E L K S S Y E L Q L T A S D M G V P Q	225
CGG GAG CTG AAG TCA AGC TAC GAG CTT CAG CTC ACT GCC TCA GAC ATG GGA GTA CCT CAG	1050
R S G S S I L K I S I S D S N D N S P A	245
AGG TCT GGC TCA TCC ATA CTA AAA ATA AGC ATT TCA GAC TCC AAT GAC AAC AGC CCT GCT	1110

Fig. 1B

F E Q Q S Y I I Q L L E N S P V G T L L 265  
 TTT GAG CAG CAA TCT TAT ATA ATA CAA CTC TTA GAA AAC TCC CCG GTT GGC ACT TTG CTC 1170  
  
 L D L N A T D P D E G A N G K I V Y S F 285  
 TTA GAT CTG AAT GCC ACG GAT CCA GAT GAG GGC GCT AAT GGG AAA ATT GTA TAT TCC TTC 1230  
  
 S S H V S P K I M E T F K I D S E R G H 305  
 AGC AGT CAT GTG TCT CCC AAA ATT ATG GAG ACT TTT AAA ATT GAT TCT GAA AGA GGA CAT 1290  
  
 L T L F K Q V D Y E I T K S Y E I D V Q 325  
 TTG ACT CTT TTC AAG CAA GTG GAT TAT GAA ATC ACC AAA TCC TAT GAG ATT GAT GTT CAG 1350  
  
 A Q D L G P N S I P A H C K I I I K V V 345  
 GCT CAA GAT TTG GGT CCA AAT TCA ATC CCA GCC CAT TGC AAA ATT ATA ATT AAG GTT GTG 1410  
  
 D V N D N K P E I N I N L M S P G K E E 365  
 GAT GTT AAT GAC AAT AAA CCT GAA ATT AAC ATC AAC CTC ATG TCC CCT GGA AAA GAA GAA 1470  
  
 I S Y I F E G D P I D T F V A L V R V Q 385  
 ATA TCT TAT ATT TTT GAA GGG GAT CCT ATT GAT ACA TTT GTT GCT TTG GTC AGA GTT CAG 1530  
  
 D K D S G L N G E I V C K L H G H F 405  
 GAC AAG GAT TCT GGG CTG AAT GGA GAA ATA GTT TGT AAG CTT CAT GGA CAT GGT CAC TTT 1590

3/361

Fig. 1C

# Sequence

K	L	Q	K	T	Y	E	N	N	Y	L	I	L	T	N	A	T	L	D	R	425
AAA	CTT	CAG	AAG	ACA	TAT	GAA	AAC	AAT	TAT	TTA	ATC	TTA	ACT	AAT	GCC	ACA	CTG	GAT	AGA	1650
E	K	R	S	E	Y	S	L	T	V	I	A	E	D	R	G	T	P	S	L	445
GAA	AAG	AGA	TCT	GAG	TAT	AGT	TTG	ACT	GTA	ATC	GCT	GAG	GAC	AGG	GGG	ACA	CCC	AGT	CTC	1710
S	T	V	K	H	F	T	V	Q	I	N	D	I	N	D	N	P	P	H	F	465
TCT	ACA	GTG	AAA	CAT	TTT	ACA	GTT	CAA	ATC	AAT	GAT	ATC	AAT	GAC	AAT	CCA	CCC	CAC	TTC	1770
Q	R	S	R	Y	E	F	V	I	S	E	N	N	S	P	G	A	Y	I	T	485
CAG	AGA	AGC	CGA	TAT	GAA	TTT	GTA	ATT	TCA	GAA	AAT	AAC	TCA	CCA	GGG	GCA	TAT	ATC	ACC	1830
T	V	T	A	T	D	P	D	L	G	E	N	G	Q	V	T	Y	T	I	L	505
ACT	GTT	ACA	GCC	ACA	GAT	CCT	GAT	CTT	GGA	GAA	AAT	GGG	CAA	GTG	ACA	TAC	ACC	ATC	TTG	1890
E	S	F	I	L	G	S	S	I	T	Y	T	V	T	I	D	P	S	N	G	525
GAG	AGT	TTT	ATT	CTA	GGA	AGT	TCC	ATA	ACT	ACA	TAT	GTA	ACC	ATT	GAC	CCA	TCT	AAT	GGA	1950
A	I	Y	A	L	R	I	F	D	H	E	E	V	S	Q	I	T	F	V	V	545
GCC	ATC	TAT	GCC	CTC	AGA	ATC	TTT	GAT	CAT	GAA	GAA	GTG	AGT	CAG	ATC	ACT	TTT	GTG	GTA	2010
E	A	R	D	G	G	S	P	K	Q	L	V	S	N	T	T	V	V	L	T	565
GAA	GCA	AGA	GAT	GGA	GGA	AGC	CCG	AAG	CAA	CTG	GTA	AGC	AAT	ACC	ACA	GTT	GTG	CTC	ACC	2070

Fig. 1D



[illegible]

I	I	D	E	N	D	N	V	P	V	I	G	P	A	L	R	N	N	T	585	
ATC	ATT	GAC	GAA	AAT	GAC	AAC	GTT	CCT	GTG	GTT	ATA	GGG	CCT	GCA	TTG	CGT	AAT	AAT	ACG	2130
A	E	I	T	I	P	K	G	A	E	S	G	F	H	V	T	R	I	R	A	605
GCA	GAA	ATC	ACC	ATT	CCC	AAA	GGG	GCT	GAA	AGT	GGC	TTT	CAT	GTC	ACA	AGA	ATA	AGG	GCA	2190
I	D	R	D	S	G	V	N	A	E	L	S	C	A	I	V	A	G	N	E	625
ATT	GAC	AGA	GAC	TCT	GGT	GTG	AAT	GCT	GAA	CTC	AGC	TGC	GCC	ATA	GTA	GCA	GGT	AAT	GAG	2250
E	N	I	F	I	I	D	P	R	S	C	D	I	H	T	N	V	S	M	D	645
GAG	AAT	ATC	TTC	ATA	ATT	GAT	CCA	CGA	TCA	TGT	GAC	ATC	CAT	ACC	AAC	GTT	AGC	ATG	GAT	2310
S	V	P	Y	T	E	W	E	L	S	V	I	I	Q	D	K	G	N	P	Q	665
TCT	GTT	CCC	TAC	ACA	GAA	TGG	GAG	CTG	TCA	GTT	ATC	ATT	CAG	GAC	AAA	GGC	AAT	CCT	CAG	2370
L	H	T	K	V	L	L	K	C	M	I	F	E	Y	A	E	S	V	T	S	685
CTA	CAT	ACC	AAA	GTC	CTT	CTG	AAG	TGC	ATG	ATC	TTT	GAA	TAT	GCA	GAG	TCG	GTG	ACA	AGT	2430
T	A	M	T	S	V	S	Q	A	S	L	D	V	S	M	I	I	I	I	S	705
ACA	GCA	ATG	ACT	TCA	GTA	AGC	CAG	GCA	TCC	TTG	GAT	GTC	TCC	ATG	ATA	ATA	ATT	ATT	TCC	2490
L	G	A	I	C	A	V	L	L	V	I	M	V	L	F	A	T	R	C	N	725
TTA	GGA	GCA	ATT	TGT	GCA	GTG	TTG	CTG	GTT	ATT	ATG	GTG	CTA	TTT	GCA	ACT	AGG	TGT	AAC	2550

R E K K D T R S Y N C R V A E S T Y Q H 745  
 CGC GAG AAG AAA GAC ACT AGA TCC TAT AAC TGC AGG GTG GCC GAA TCA ACT TAC CAG CAC 2610

H P K R P S R Q I H K G D I T L V P T I 765  
 CAC CCA AAA AGG CCA TCC CGG CAG ATT CAC AAA GGG GAC ATC ACA TTG GTG CCT ACC ATA 2670

N G T L P I R S H H R S S P S S S P T L 785  
 AAT GGC ACT CTG CCC ATC AGA TCT CAT CAC AGA TCG TCT CCA TCT TCA TCT CCT ACC TTA 2730

E R G Q M G S R Q S H N S H Q S L N S L 805  
 GAA AGA GGG CAG ATG GGC AGC CGG CAG AGT CAC AAC AGT CAC CAG TCA CTC AAC AGT TTG 2790

V T I S S N H V P E N F S L E L T H A T 825  
 GTG ACA ATC TCA TCA AAC CAC CAC GTG CCA GAG AAT TTC TCA TTA GAA CTC ACC CAC GCC ACT 2850

P A V E Q V S Q L L S M L H Q Q G Q Y Q P 845  
 CCT GCT GTT GAG CAG GTC TCT CAG CTT CTT TCA ATG CTT CAC CAG GGG CAA TAT CAG CCA 2910

R P S F R G N K Y S R S Y R Y A L Q D M 865  
 AGA CCA AGT TTT CGA GGA AAC AAA TAT TCC AGG AGC TAC AGA TAT GCC CTT CAA GAC ATG 2970

D K F S L K D S G R G D S E A G D S D Y 885  
 GAC AAA TTT AGC TTG AAA GAC AGT GGC CGT GGT GAC AGT GAG GCA GGA GAC AGT GAT TAT 3030

D	L	G	R	D	S	P	I	D	R	L	L	G	E	G	F	S	D	L	F	905
GAT	TTG	GGG	CGA	GAT	TCT	CCA	ATA	GAT	AGG	CTG	CTG	GGT	GAA	GGA	TTC	AGC	GAC	CTG	TTT	3090
L	T	D	G	R	I	P	A	A	M	R	L	C	T	E	E	C	R	V	L	925
CTC	ACA	GAT	GGA	AGA	ATT	CCA	GCA	GCT	ATG	AGA	CTC	TGC	ACG	GAG	GAG	TGC	AGG	GTC	CTG	3150
G	H	S	D	Q	C	W	M	P	P	L	P	S	P	S	S	D	Y	R	S	945
GGA	CAC	TCT	GAC	CAG	TGC	TGG	ATG	CCA	CCA	CTG	CCC	TCA	CCG	TCT	TCT	GAT	TAT	AGG	AGT	3210
N	M	F	I	P	G	E	E	F	P	T	Q	P	Q	Q	Q	H	P	H	Q	965
AAC	ATG	TTC	ATT	CCA	GGG	GAA	GAA	TTC	CCA	ACG	CAA	CCC	CAG	CAG	CAG	CAT	CCA	CAT	CAG	3270
S	L	E	D	D	A	Q	P	A	D	S	G	E	K	K	K	S	F	S	T	985
AGT	CTT	GAG	GAT	GAC	GCT	CAG	CCT	GCA	GAT	TCC	GGT	GAA	AAG	AAG	AAG	AGT	TTT	TCC	ACC	3330
F	G	K	D	S	P	N	D	E	D	T	G	D	T	S	T	S	S	L	L	1005
TTT	GGA	AAG	GAC	TCC	CCA	AAC	GAT	GAG	GAC	ACT	GGG	GAT	ACC	AGC	ACA	TCA	TCT	CTG	CTC	3390
S	E	M	S	S	V	F	Q	R	L	L	P	P	S	L	D	T	Y	S	E	1025
TCG	GAA	ATG	AGC	AGT	GTG	TTC	CAG	CGT	CTC	TTA	CCG	CCT	TCC	CTG	GAC	ACC	TAT	TCT	GAA	3450
C	S	E	V	D	R	S	N	S	L	E	R	R	K	G	P	L	P	A	K	1045
TGC	AGT	GAG	GTG	GAT	CGG	TCC	AAC	TCC	CTG	GAG	CGC	AGG	AAG	GGA	CCC	TTG	CCA	GCC	AAA	3510

7/361

[illegible]

T	T	N	C	G	P	P	L	G	T	H	S	V	Q	P	S	S	K	'W		1085
ACC	ACC	AAC	TGT	GGG	CCG	CCA	CTT	GGA	ACT	CAC	TCC	AGT	GTG	CAG	CCT	TCT	TCA	AAA	TGG	3630

L	P	A	M	E	E	I	P	E	N	Y	E	D	F	D	N	V	L	1105		
CTG	CCA	GCC	ATG	GAG	GAG	ATC	CCT	GAA	AAT	TAT	GAG	GAA	GAT	GAT	TTT	GAC	AAT	GTG	CTC	3690

[illegible]

N	K	L	I	Q	D	V	R	Q	S	*
AAC	AAA	CTG	CTT	CAA	GAT	GTC	CGC	CAG	AGC	TAG

GAGATTTAGCGAAGCATTTTGTTCATGTATATGGAATAGGGAACAACAACAACAAAAACCTGAAAGAAC 3862  
 TGGCATTGCCAAATAGTTGCATTTATCATAAATGTGCTGTGTATATTGAAATATTAAATACTGTATTTTCGTATGTACA 3941  
 CAATGCAAGTGTATATTTTAAATCTGTATTTTAAAAATACATTTGTACCTTATATTTATGTGTAAATTTAACAAACAAA 4020  
 TTTTATTTTCTACTCCCATGACAGACATGTTTTTCCTAGTCGTAGAAACTAGCCACTGTTCAAATCTGATACACTA 4099  
 TTCAACCACAAGTGTAAAGGCACCTGCTTAGATTAGTTTGTGTTGGGAAGAAATTATTA TGTGTATGAACAACCCCACT 4178  
 EAAGCATTATACAATTCTTAATCCATTAAAGTGATCCCACTTTTTCAAATAACTTTTTAGAAATTAAGAAATCATTAA 4257  
 ATTGTTAAGCTATTTATTGTTATTTTCTCTACTTTCTACTAGCCCCAAATAGTTGAACCTCTTATAGGAAAAATCGAAAGA 4336  
 TAAAGTGAAGTTTATTTACGACCTGAGAAATATCTTGAAGTTATTATTATAGATGACTATCTCAAATGAACTTTTAT 4415

**Fig. 1H.**

AGACAAATGATGAAAAACAGAACTAAAGTCAATGTTTCTGACTCCCAGGCCCTACTATTCCAGGCCATCACACTGGCCT 4494  
GTTCCGGAGAAATATTTCTCTCACAAATATTTATCTACTTATAATTATGGTAAACAATAAATTTTATTCATCCTTGTA 4573  
GTATGAAACATGCTCCAAGGAAATCTGTCCTTTAAATGGATAACAGTATGTGTTCTAAATGGCATAAAATATTAC 4652  
TGGATAAAAAACAGTTGTGTGTCCTCTCCTAAGGTAGTAAATATAAATTGACTTATCTGAAACCCATTCTATTTTGAA 4731  
TCTCCCTTTCTCTCACAAATCTTGAAACATTTTAATCTTTTGGAAATATTGTCTTTCTTTGTTATAACTATTTCATTTT 4810  
AGCTTTTGTCTCCAGTGCA TGATCTCATATTTTGTCTTTTATTTTGTAGTATAAGAACATTTATAAAAATCATATTTTGT 4889  
TACTGCAATTGTTTATTTGTTGTGGCAAAATGAGAAAATCCTTTATTTATTTGTGCTGTGATCTCTCTGTGTGGAATGC 4968  
CTTGTGAGAGAGATGCTTATTAATGACTATTATCAATTTCTGACCAAGCTTCTATTAATGTTATTTCTAAATAACACTA 5047  
TCTTGATTGTA CTCTCCAGAAAAATTTTCTGTGCAGTGAAAAATAAAAGAAAAATTAAGTAAAAAATAAAAAA 5121

**Fig. 11**



I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	930
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	CTC	AGA	GAG	TTA	GAT	990
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110
F	E	Q	Q	S	Y	I	I	Q	L	L	E	N	S	P	V	G	T	L	L	265
TTT	GAG	CAG	CAA	TCT	TAT	ATA	ATA	CAA	CTC	TTA	GAA	AAC	TCC	CCG	GTT	GGC	ACT	TTG	CTC	1170



L D L N A T D P D E G A N G K I V Y S F 285  
 TTA GAT CTG AAT GCC ACG GAT CCA GAT GAG GGC GCT AAT GGG AAA ATT GTA TAT TCC TTC 1230  
  
 S S H V S P K I M E T F K I D S E R G H 305  
 AGC AGT CAT GTG TCT CCC AAA ATT ATG GAG ACT TTT AAA ATT GAT TCT GAA AGA GGA CAT 1290  
  
 L T L F K Q V D Y E I T K S Y E I D V Q 325  
 TTG ACT CTT TTC AAG CAA GTG GAT TAT GAA ATC ACC AAA TCC TAT GAG ATT GAT GTT CAG 1350  
  
 A Q D L G P N S I P A H C K I I I K V V 345  
 GCT CAA GAT TTG GGT CCA AAT TCA ATC CCA GCC CAT TGC AAA ATT ATA ATT AAG GTT GTG 1410  
  
 D V N D N K P E I N I N L M S P G K E E 365  
 GAT GTT AAT GAC AAT AAA CCT GAA ATT AAC ATC AAC CTC ATG TCC CCT GGA AAA GAA GAA 1470  
  
 I S Y I F E G D P I D T F V A L V R V Q 385  
 ATA TCT TAT ATT TTT GAA GGG GAT CCT ATT GAT ACA TTT GTT GCT TTG GTC AGA GTT CAG 1530  
  
 D K D S G L N G E I V C K L H G H G H F 405  
 GAC AAG GAT TCT GGG CTG AAT GGA GAA ATA GTT TGT AAG CTT CAT GGA CAT GGT CAC TTT 1590  
  
 K L Q K T Y E N N Y L I L T N A T L D R 425  
 AAA CTT CAG AAG ACA TAT GAA AAC AAT TAT TTA ATC TTA ACT AAT GCC ACA CTG GAT AGA 1650

12/361

Fig. 2C



E K R S E Y S L T V I A E D R G T P S L 445  
 GAA AAG AGA TCT GAG TAT AGT TTG ACT GTA ATC GCT GAG GAC AGG GGG ACA CCC AGT CTC 1710  
  
 S T V K H F T V Q I N D I N D N P P H F 465  
 TCT ACA GTG AAA CAT TTT ACA GTT CAA ATC AAT GAT ATC AAT GAC AAT CCA CCC CAC TTC 1770  
  
 Q R S R Y E F V I S E N N S P G A Y I T 485  
 CAG AGA AGC CGA TAT GAA TTT GTA ATT TCA GAA AAT AAC TCA CCA GGG GCA TAT ATC ACC 1830  
  
 T V T A T D P D L G E N G Q V T Y T I L 505  
 ACT GTT ACA GCC ACA GAT CCT GAT CTT GGA GAA AAT GGG CAA GTG ACA TAC ACC ATC TTG 1890  
  
 E S F I L G S S I T T Y V T I D P S N G 525  
 GAG AGT TTT ATT CTA GGA AGT TCC ATA ACT ACA TAT GTA ACC ATT GAC CCA TCT AAT GGA 1950  
  
 A I Y A L R I F D H E E V S Q I T F V V 545  
 GCC ATC TAT GCC CTC AGA ATC TTT GAT CAT GAA GAA GTG AGT CAG ATC ACT TTT GTG GTA 2010  
  
 E A R D G G S P K Q L V S N T T V V L T 565  
 GAA GCA AGA GAT GGA GGA AGC CCG AAG CAA CTG GTA AGC AAT ACC ACA GTT GTG CTC ACC 2070  
  
 I I D E N D N V P V V I G P A L R N N T 585  
 ATC ATT GAC GAA AAT GAC AAC GTT CCT GTG GTT ATA GGG CCT GCA TTG CGT AAT AAT ACG 2130

Fig. 2D

A E I T I P K G A E S G F H V T R I R A 605  
 GCA GAA ATC ACC ATT CCC AAA GGG GCT GAA AGT GGC TTT CAT GTC ACA AGA ATA AGG GCA 2190  
  
 I D R D S G V N A E L S C A I V A G N E 625  
 ATT GAC AGA GAC TCT GGT GTG AAT GCT GAA CTC AGC TGC GCC ATA GTA GCA GGT AAT GAG 2250  
  
 E N I F I I D P R S C D I H T N V S M D 645  
 GAG AAT ATC TTC ATA ATT GAT CCA CGA TCA TGT GAC ATC CAT ACC AAC GTT AGC ATG GAT 2310  
  
 S V P Y T E W E L S V I I Q D K G N P Q 665  
 TCT GTT CCC TAC ACA GAA TGG GAG CTG TCA GTT ATC ATT CAG GAC AAA GGC AAT CCT CAG 2370  
  
 L H T K V L L K C M I F E Y A E S V T S 685  
 CTA CAT ACC AAA GTC CTT CTG AAG TGC ATG ATC TTT GAA TAT GCA GAG TCG GTG ACA AGT 2430  
  
 T A M T S V S Q A S L D V S M I I I S 705  
 ACA GCA ATG ACT TCA GTA AGC CAG GCA TCC TTG GAT GTC TCC ATG ATA ATA ATT ATT TCC 2490  
  
 L G A I C A V L L V I M V L F A T R C N 725  
 TTA GGA GCA ATT TGT GCA GTG TTG CTG GTT ATT ATG GTG CTA TTT GCA ACT AGG TGT AAC 2550  
  
 R E K K D T R S Y N C R V A E S T Y Q H 745  
 CGC GAG AAG AAA GAC ACT AGA TCC TAT AAC TGC AGG GTG GCC GAA TCA ACT TAC CAG CAC 2610

Fig. 2E



# TABLE 2

L	T	D	G	R	I	P	A	A	M	R	L	C	T	E	E	C	R	V	L	924
CTC	ACA	GAT	GGA	AGA	ATT	CCA	GCA	GCT	ATG	AGA	CTC	TGC	ACG	GAG	GAG	TGC	AGG	GTC	CTG	3147
G	H	S	D	Q	C	W	M	P	P	L	P	S	P	S	S	D	Y	R	S	944
GGA	CAC	TCT	GAC	CAG	TGC	TGG	ATG	CCA	CCA	CTG	CCC	TCA	CCG	TCT	TCT	GAT	TAT	AGG	AGT	3207
N	M	F	I	P	G	E	E	F	P	T	Q	P	Q	Q	Q	H	P	H	Q	964
AAC	ATG	TTC	ATT	CCA	GGG	GAA	GAA	TTC	CCA	ACG	CAA	CCC	CAG	CAG	CAG	CAT	CCA	CAT	CAG	3267
S	L	E	D	D	A	Q	P	A	D	S	G	E	K	K	K	S	F	S	T	984
AGT	CTT	GAG	GAT	GAC	GCT	CAG	CCT	GCA	GAT	TCC	GGT	GAA	AAG	AAG	AAG	AGT	TTT	TCC	ACC	3327
F	G	K	D	S	P	N	D	E	D	T	G	D	T	S	T	S	S	L	L	1004
TTT	GGA	AAG	GAC	TCC	CCA	AAC	GAT	GAG	GAC	ACT	GGG	GAT	ACC	AGC	ACA	TCA	TCT	CTG	CTC	3387
S	E	M	S	S	V	F	Q	R	L	L	P	P	S	L	D	T	Y	S	E	1024
TCG	GAA	ATG	AGC	AGT	GTG	TTC	CAG	CGT	CTC	TTA	CCG	CCT	TCC	CTG	GAC	ACC	TAT	TCT	GAA	3447
C	S	E	V	D	R	S	N	S	L	E	R	R	K	G	P	L	P	A	K	1044
TGC	AGT	GAG	GTG	GAT	CGG	TCC	AAC	TCC	CTG	GAG	CGC	AGG	AAG	GGA	CCC	TTG	CCA	GCC	AAA	3507
T	V	G	Y	P	Q	G	V	A	A	W	A	A	S	T	H	F	Q	N	P	1064
ACT	GTG	GGT	TAC	CCA	CAG	GGG	GTA	GCG	GCA	TGG	GCA	GCC	AGT	ACG	CAT	TTT	CAA	AAT	CCC	3567

Fig. 2G

T T N C G P P L G T H S S V Q P S S K W 1084  
ACC ACC AAC TGT GGG CCG CCA CTT GGA ACT CAC TCC AGT GTG CAG CCT TCT TCA AAA TGG 3627

L P A M E E I P E N Y E D D F D N V L 1104  
CTG CCA GCC ATG GAG GAG ATC CCT GAA AAT TAT GAG GAA GAT GAT TTT GAC AAT GTG CTC 3687

N H L N D G K H E L M D A S E L V A E I 1124  
AAC CAC CTC AAT GAT GGG AAA CAC GAA CTC ATG GAT GCC AGT GAA CTG GTG GCA GAG ATT 3747

N K L L Q D V R Q S \* 1134  
AAC AAA CTG CTT CAA GAT GTC CGC CAG AGC TAG 3780

17/361

GAGATTTAGCGAAGCATTTTGTTCATGTATATGGAATAGGGAACAACAACAACAAAAACCCCTGAAAGAAC 3859  
TGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTCTGTATATTTGAATATTTAAATACTGTATTTTCGTATGTACA 3938  
CAATGCAAGTGTGATTATTTAATCTGTATTTTAAATAACATTTGTACCTTATATTTATGTGTAAATTTAACAAACAAA 4017  
TTTTATTTTTTTACTCCCATGACAGACATGTTTTTCCCTAGTCGTAGAAACTAGCCACTGTTCAAATCTGATACACTA 4096  
TTCAACCACAAAGTGTAAGGCCACTGCTTAGATTAGTTTTTGTGGGAAGAAATTAATATGTTGTATGAACAACCCCACT 4175  
GAAGCATTATACAAATTCCTTAATTCATTAAGTGATCCCACTTTTTTCAATAAATTTTAGAAAATTAAGAAATCATTTAA 4254  
ATTGTTAAGCTATTTTATTTGTTATTTCTCTACTTTCTACTAGCCCCCAATAGTTGAACCTCTTATAGGAAAATCGAAAAGA 4333  
TAAAGTAAAAGTTTATTTTCAGGACTGAGAAAATATCTTGAAGGTTATTTATTAGATGACTATCTCAAAATGAACCTTTTAT 4412  
AGACAAATGATGAAAACAGAACTAAAGTCAATGTTTCCCTGACTCCCGCCCTACTATTTCCAGGCCATCACACTGGCCT 4491  
GTTCCGGAGAATATTTCTCTCAAAATATATATCTACTTATAAATTAATGTAACAATAAATTTTATTCATCCTTGTA 4570  
GTATGAAACATGCTCCAAGGAAATCTGTCCTTTAAATGATAACAGTATGTGTCTAATGTCATAAAATATTAC 4649  
TGGATAAAAACAGTTGTGTGTCCTCCTAAGGTAGTAAATATAATTGACTTATTTCTGAACCCATCTCTATTGAA 4728

Fig. 2H

TCTCCCCCTTCCCTCACAATACTTGAAACATTTTAATCTTTTGGAATATTGTCTTTCTTTGTTATAACTATTTCATTTT 4807  
 AGCTTTTGTCTCCAGTGCATGATCTCATATTTTGTGCTTTTATTTTAGTATAAGAACATTTATAAAATCATAATTTTGT 4886  
 TACTGCAATTGTTTATTGTTGTGGCAAAATGAGAAATCCCTTTATTTATTGCTGTGATCTCTCTGTGGAAATGC 4965  
 CTTGGTGAGAGAGATGCTTATTATGACTATTATCATTTCTGACCAAGCTTCTATTAAATGTTATTTCTAAATAATACACTA 5044  
 TCTTGATTGTACTCTCCAGAAAATTTTCTGTCTGAGTGAATAAAAGAAAAATTAAGTAAAAAATAAAAAA 5118

Fig. 2I

T416	1651	GAAAAGAGATCTGAGTATAGTTTGACTGTAAATCGCTGAGGACAGGGGGAC	1700
AL137471	1	...AAGAGATCTGAGTATAGTTTGACTGTAAATCGCTGAGGACAGGGGGAC	47
T416	1701	ACCCAGTCTCTCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA	1750
AL137471	48	ACCCAGTCTCTCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA	97
T416	1751	ATGACAAATCCACCCCACTTCCAGAGAGCCGATATGAAATTTGTAAATTCA	1800
AL137471	98	ATGACAAATCCACCCCACTTCCAGAGAGCCGATATGAAATTTGTAAATTCA	147
T416	1801	GAAAATAACTCACAGGGGCATATATCACCACTGTACAGCCACAGATCC	1850
AL137471	148	GAAAATAACTCACAGGGGCATATATCACCACTGTACAGCCACAGATCC	197
T416	1851	TGATCTTGGAGAAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTTA	1900
AL137471	198	TGATCTTGGAGAAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTTA	247
T416	1901	TTCTAGGAAGTTCCATAACTACATATGTAAACCATTGACCCATCTAATGGA	1950
AL137471	248	TTCTAGGAAGTTCCATAACTACATATGTAAACCATTGACCCATCTAATGGA	297

FIG. 4A

T416	1951	GCCATCTATGCCCTCAGAAATCTTTGATCATGAAGAAGTGAGTCAGATCAC	2000
AL137471	298	GCCATCTATGCCCTCAGAAATCTTTGATCATGAAGAAGTGAGTCAGATCAC	347
T416	2001	TTTTGTGTAGAAGCAAGAGATGGAGGAAAGCCCGAAGCAACTGGTAAGCA	2050
AL137471	348	TTTTGTGTAGAAGCAAGAGATGGAGGAAAGCCCGAAGCAACTGGTAAGCA	397
T416	2051	ATACCACAGTTGTGCTCACCATCATTTGACGAAAAATGACAAACGTTCCCTGTG	2100
AL137471	398	ATACCACAGTTGTGCTCACCATCATTTGACGAAAAATGACAAACGTTCCCTGTG	447
T416	2101	GTTATAGGGCCTGCATTGCGTAATAATACGGCAGAAATCACCATTCCCAA	2150
AL137471	448	GTTATAGGGCCTGCATTGCGTAATAATACGGCAGAAATCACCATTCCCAA	497
T416	2151	AGGGGCTGAAAAGTGGCTTTTCATGTCAACAAGAAATAAGGGCAATTGACAGAG	2200
AL137471	498	AGGGGCTGAAAAGTGGCTTTTCATGTCAACAAGAAATAAGGGCAATTGACAGAG	547
T416	2201	ACTCTGGTGTGAATGCTGAACTCAGCTGCGCCCATAGTAGCAGGTAATGAG	2250
AL137471	548	ACTCTGGTGTGAATGCTGAACTCAGCTGCGCCCATAGTAGCAGGTAATGAG	597

FIG. 4B



T416	2251	GAGAAATATCTTCATAAATTGATCCACGATCATGTGACATCCATACCAACGT	2300
AL137471	598	GAGAAATATCTTCATAAATTGATCCACGATCATGTGACATCCATACCAACGT	647
T416	2301	TAGCATGGATTCTGTTCCTACACAGAAATGGAGCTGTGAGTTATCATTC	2350
AL137471	648	TAGCATGGATTCTGTTCCTACACAGAAATGGAGCTGTGAGTTATCATTC	697
T416	2351	AGGACAAAGGCAATCCTCAGCTACATACCAAAAGTCCCTTCTGAAGTGCAATG	2400
AL137471	698	AGGACAAAGGCAATCCTCAGCTACATACCAAAAGTCCCTTCTGAAGTGCAATG	747
T416	2401	ATCTTTGAATATGCAGAGTCGGTGACAAAGTACAGCAATGACTTCAGTAAG	2450
AL137471	748	ATCTTTGAATATGCAGAGTCGGTGACAAAGTACAGCAATGACTTCAGTAAG	797
T416	2451	CCAGGCATCCTTGGATGTCTCCATGATAATAATTATTTCCCTTAGGAGCAA	2500
AL137471	798	CCAGGCATCCTTGGATGTCTCCATGATAATAATTATTTCCCTTAGGAGCAA	847
T416	2501	TTTGTGCAGTGTGCTGGTTATTATGGTGCTATTTCGCAACTAGGTGTAAC	2550
AL137471	848	TTTGTGCAGTGTGCTGGTTATTATGGTGCTATTTCGCAACTAGGTGTAAC	897

FIG. 4C

T416	2551	CGCGAGAAAGACACTAGATCCTATAACTGCAGGGTGGCCGGAATCAAC	2600
AL137471	898	CGCGAGAAAGACACTAGATCCTATAACTGCAGGGTGGCCGGAATCAAC	947
T416	2601	TTACCAGCACCAACCAAAAGGCCATCCCGGCAGATTCACAAAGGGGACA	2650
AL137471	948	TTACCAGCACCAACCAAAAGGCCATCCCGGCAGATTCACAAAGGGGACA	997
T416	2651	TCACATTGGTGCCCTACCATAAAATGGCACTCTGCCCATCAGATCTCATCAC	2700
AL137471	998	TCACATTGGTGCCCTACCATAAAATGGCACTCTGCCCATCAGATCTCATCAC	1047
T416	2701	AGATCGTCTCCATCTTCATCTCCTACCTTAGAAAGAGGCAGATGGGCAG	2750
AL137471	1048	AGATCGTCTCCATCTTCATCTCCTACCTTAGAAAGAGGCAGATGGGCAG	1097
T416	2751	CCGGCAGAGTCACAACAGTCACCAGTCACCTCAACAGTTTGGTGACAATCT	2800
AL137471	1098	CCGGCAGAGTCACAACAGTCACCAGTCACCTCAACAGTTTGGTGACAATCT	1147
T416	2801	CATCAAAACCAACGTGCCAGAGAAATTTCTCATTTAGAACTCACCCACGCCACT	2850
AL137471	1148	CATCAAAACCAACGTGCCAGAGAAATTTCTCATTTAGAACTCACCCACGCCACT	1197

FIG. 4D

T416	2851	CCTGCTGTGAGCAGGTCTCTCAGCTTCTTTCAATGCTTCAACAGGGCA	2900
AL137471	1198	CCTGCTGTGAGCAGGTCTCTCAGCTTCTTTCAATGCTTCAACAGGGCA	1247
T416	2901	ATATCAGCCAAGACCAAGTTTTCGAGGAAACAAATATTCAGGAGCTACA	2950
AL137471	1248	ATATCAGCCAAGACCAAGTTTTCGAGGAAACAAATATTCAGGAGCTACA	1297
T416	2951	GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGGCCGT	3000
AL137471	1298	GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGGCCGT	1347
T416	3001	GGTGACAGTGAGGCAGGAGACAGTGATTAATGATTGGGGCGAGATTCTCC	3050
AL137471	1348	GGTGACAGTGAGGCAGGAGACAGTGATTAATGATTGGGGCGAGATTCTCC	1397
T416	3051	AATAGATAGGCTGCTGGGTGAAGGATTCAGCGACCTGTTTCTCACAGATG	3100
AL137471	1398	AATAGATAGGCTGCTGGGTGAAGGATTCAGCGACCTGTTTCTCACAGATG	1447
T416	3101	GAAGAATTCAGCAGCTATGAGACTCTGCACGGAGAGTGCAGGGTCCCTG	3150
AL137471	1448	GAAGAATTCAGCAGCTATGAGACTCTGCACGGAGAGTGCAGGGTCCCTG	1497

FIG. 4E

T416	3151	GGACACTCTGACCAGTGTGGATGCCACCACCTGCCCTCACCGTCTTCTGA	3200
AL137471	1498	GGACACTCTGACCAGTGTGGATGCCACCACCTGCCCTCACCGTCTTCTGA	1547
T416	3201	TTATAGGAGTAACATGTTTCATTCAGGGGAAGAATTCCCAACGCAACCCC	3250
AL137471	1548	TTATAGGAGTAACATGTTTCATTCAGGGGAAGAATTCCCAACGCAACCCC	1597
T416	3251	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	3300
AL137471	1598	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	1647
T416	3301	TCCGGTGAAAAGAAAGAGTTTTCACCTTTGGAAAAGGACTCCCCAAA	3350
AL137471	1648	TCCGGTGAAAAGAAAGAGTTTTCACCTTTGGAAAAGGACTCCCCAAA	1697
T416	3351	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAAATGA	3400
AL137471	1698	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAAATGA	1747
T416	3401	GCAGTGTGTTCCAGCGTCTCTTACCGCCTTCCCTGGACACCTATTCTGAA	3450
AL137471	1748	GCAGTGTGTTCCAGCGTCTCTTACCGCCTTCCCTGGACACCTATTCTGAA	1797

FIG. 4F

T416	3451	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCCCTT	3500
AL137471	1798	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCCCTT	1847
T416	3501	GCCAGCCAAAACCTGTGGGTACCCACAGGGGTAGCGGCATGGGCAGCCA	3550
AL137471	1848	GCCAGCCAAAACCTGTGGGTACCCACAGGGGTAGCGGCATGGGCAGCCA	1897
T416	3551	GTACGCATTTTCAAAAATCCCAACCACTGTGGGCCGCCACTTGGAACCT	3600
AL137471	1898	GTACGCATTTTCAAAAATCCCAACCACTGTGGGCCGCCACTTGGAACCT	1947
T416	3601	CACTCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	3650
AL137471	1948	CACTCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	1997
T416	3651	CCCTGAAAAATTATGAGGAAGATGATTTTGACAAATGTGTCTCAACCACTCA	3700
AL137471	1998	CCCTGAAAAATTATGAGGAAGATGATTTTGACAAATGTGTCTCAACCACTCA	2047
T416	3701	ATGATGGGAAACACGAACTCATGGATGCCAGTGAACTGGTGGCAGAGATT	3750
AL137471	2048	ATGATGGGAAACACGAACTCATGGATGCCAGTGAACTGGTGGCAGAGATT	2097

FIG. 4G

T416 3751 AACAACTGCTTCAAGATGTCCGCCAGAGCTAGGAGATTTTAGCGAAGCA 3800  
 AL137471 2098 AACAACTGCTTCAAGATGTCCGCCAGAGCTAGGAGATTTTAGCGAAGCA 2147  
 T416 3801 TTTTGTTCATGTATATGGAAATAGGGAACAACAACAACAAAAA 3850  
 AL137471 2148 TTTTGTTCATGTATATGGAAATAGGGAACAACAACAACAAAAA 2197  
 T416 3851 CCCTGAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC 3900  
 AL137471 2198 CCCTGAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC 2247  
 T416 3901 TGTGTATATTGAATATTAAATACTGTATTTTCGTATGTACACAATGCAAG 3950  
 AL137471 2248 TGTGTATATTGAATATTAAATACTGTATTTTCGTATGTACACAACAAAAA 2297  
 T416 3951 TGTGATTATTTTAACTCTGTATTTTAAAAATACATTTGTACCTTATATTA 4000  
 AL137471 2298 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG..... 2338

FIG. 4H

T416	1	..ATGCACCAAATG..AATGCTAAAAATGCACCTTTAGGTTTGTTTTGCA	45
m-PC	1	ATGATGCTACTTCTGCCATTCTGCTAGGGCTCTTAGGGCCAGGAAGCTA	50
T416	46	CTTCTGATAGTATCTTTCAACCACGATGTACTGGGCA...AGAAATTGAA	92
m-PC	51	CT..TGTTCAATTCAGGGGATTGTCAGGAGGTGGCCACTGTCA TGGTGAA	98
T416	93	ATACAGGATTTATGAGGAACAGAGGGTTGGATCAGTAATTGCAAGACTAT	142
m-PC	99	ATTCCAAGTGACAGAGGAAGTGCCGCTCTGGCACGGTGATAGGGAAACTGT	148
T416	143	CAGAGGATGTGGCTGATGTTTATTGAAGCTTCCTAATCCTTCTACTGTT	192
m-PC	149	CCCAAGAACT..AAGA.GTGGAGGAGAGGCGTGGGAAGGCAGGAGATG..	193
T416	193	CGAATTCGAGCCATGCAGAGGGGAAATTCTCCTCTACTTGTAGTAAACGA	242
m-PC	194	CCTTCCAGATTC.TGCAGCTGCCTCAGGCACTGCCGGTTCAGATGAACTC	242

FIG. 5A

T416	243	GGATAATGGGAAATCAGCATAGGGCTACAATTGACCGTGAACAACTGT	292
m-PC	243	TGAGACGGCCTGTCTCAGCACTTCCAGCCGGCTGGATCGGAGAAGCTAT	292
T416	293	GCCAGAAAACCTTGAACCTGTTCATAGAGTTTGATGTGATCACTCTACCC	342
m-PC	293	GTCGGCAGGAAGATCCCTGTCTGGTGTCAATTGACGTG.....CTTGCC	336
T416	343	ACA.GAGCATCTGCAGCTTTTCCATATTGAAGTTGAAGTCTGGATATTA	391
m-PC	337	ACAGGGCGTCTGC.TCTAATTCTGTGGAGATTTCAGGTGCTAGACATCA	385
T416	392	ATGACAAATTCTCCCCAGTTTTCAGATCTCTCATACCTATTGAGATATCT	441
m-PC	386	ATGACCACCCAGCCACAGTTTCCCAAAGACGAGCAGGAACCTGGAAATCTCA	435
T416	442	GAGAGTGCAGCAGTTGGGACTCGCATTCCTCCCTGGACAGTGCATTGATCC	491
m-PC	436	GAGAGTGCCTCTCTGCACACACGAATCCCCTTGGACAGAGCTCTTGACCA	485

FIG. 5B



T416	492	AGATGTTGGGAAATTCCTCCACACATACTCGCTCTCTGCCAATGATT	541
m-PC	486	AGACACGGGTCCTAACAGCTTATATTCCTACTCCCTGTCTCCCAAGTGAAC	535
T416	542	TTTTTAAATATCGAGGTTCCGACCAGGACTGATGGAGCCCAAGTATGCAGAA	591
m-PC	536	ACTTTGCCCTGGATGTTATTGTGGGCCCTGATGAGACCAACAATGCAGAG	585
T416	592	CTCATAGTGGTCAGAGAGTTAGATCGGGAGCTGAAAGTCAAGCTACGAGCT	641
m-PC	586	CTTGTTGGTGAAGGAGTTGGACAGGGAACCTCCACTCATAATTTGATCT	635
T416	642	TCAGCTCACTGCCTCAGAC.ATGGGAGTACCTCAGAGGTCCTGGCTCATCC	690
m-PC	636	GGTGCTGACCGCCTATGACAAATGGGAAT.CCCCCTAAGTCAGGGAATCAGC	684
T416	691	ATACTAAAAATAAGCATTTTCAGACTCCAATGACAAACAGCCCTGCTTTGA	740
m-PC	685	GTGGTCAAGGTCAATGTCTCGGACTCCAATGACAAATAGTCCAGTGTTTGC	734

FIG. 5C

T416	741	GCAGCAATCTTATATAATAACAACCTCTTAGAAAACTCCCCGGTTGGCACTT	790
m-PC	735	TGAGAGTTCAGCTAGCACTAGAAAATCCCAGAAAGACACTGTTCTCTGGTACTC	784
T416	791	TGCTCTTAGATCTGAATGCCACGGATCCAGATGAGGGCGCTAATGGGAAA	840
m-PC	785	TTCTCATAAACCTGACTGCTACAGATCCCGACCAAGGACCCCAATGGGGAG	834
T416	841	ATTGTATATTCCCTTCAGCAGTCATGTGTCTCCCAAATATATGGAGACTTT	890
m-PC	835	GTAGAGTTCTTCTTTGGCAAGCATGTGTCTCCCAAGAGGTGATGAACACCTT	884
T416	891	TAAAAATTGATTCTGAAAAGAGGACATTTGACTCTTTTCAAGCAAGTGGATT	940
m-PC	885	TGGCATAGATGCCAAGACAGGCCAGATCATTTCTGCGCCAAGCCCCTAGATT	934
T416	941	ATGAAATCACCAAAATCCCTATGAGATTGATGTTCAAGGCTCAAGATTGCGGT	990
m-PC	935	ACGAGAAGAAACCTGCCTATGAGGTGGATGTCCAGGCAAGGATTGCGGT	984

FIG. 5D

T416	991	CCAAATTCAATCCCAGCCCATTTGCAAAATTATAATTAAGGTTGTGGATGT	1040
m-PC	985	CCCAATTCCATCCCAGGCCATTGCAAAAGTTCTTATCAAAGTTCCTGGATGT	1034
T416	1041	TAATGACAATAAACCTGAAATTAAACATCAACCTCATGTCCCCTGGAAAAG	1090
m-PC	1035	CAATGACAATGCCCC.....AAGCATCCTCATCACGT...GGCCTCC	1074
T416	1091	AAGAAATATCTTATATTTTGAAGGGGATCCTATTGATACATTTGTTGCT	1140
m-PC	1075	CAGACGTCGCT..GGTGCAGAAGATCTTCCCAGGATAGCTTCATTGCC	1122
T416	1141	TTGGTCAGAGTTCAGGACAAGGATTCTGGGCTGAATGGAGAAATAGTTG	1190
m-PC	1123	CTTGTCAGTGCGAATGACTTGGACTCAGGAAACAACGGTCTCGTCCACTG	1172
T416	1191	TAAGCT...TCATGGACATGGTCACCTTTAACTTCAGAAACATATGAAA	1237
m-PC	1173	TTGGCTGAATCAAGAGCTGGGCCACTTCAGACTGAAAAGGACTAACGGCA	1222

FIG. 5E

T416	1238	ACAAATTAATTAATCTTAATACTAATGCCACACTGGATAGAGAAAAGAGATCT	1287
m-PC	1223	ACACGTACATGCTGCTCACCAATGCCACACTGGACAGAGACAGTGGCCC	1272
T416	1288	GAGTATAGTTTGACTGTAATCGCTGAGGACAGGGGACACCCAGTC..TC	1335
m-PC	1273	ATATATACTCTCACTGTGTGTGCCCCAAGAC.CAAGGAC.CCCAGCCCTTA	1320
T416	1336	TCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCAATGACAATCC	1385
m-PC	1321	TCAGCTGAGAAGGAGCTCCAAATTCAGGTTAGTGATGTCAATGACAATGC	1370
T416	1386	ACCCCACTTCCAGAGAAGCCGATATGAATTTGTAAATTCAGAAAAATAACT	1435
m-PC	1371	CCCTGTGTTTGAGAAGAGCCGGTACGAGGTCTCCACTTGGGAAAAATAACC	1420
T416	1436	CACCAGGGGCATATATCACCACCTGTTACAGCCACAGATCCTGATCTTGA	1485
m-PC	1421	CACCCCTCTCTTCACCTCATCAGCTCAAAGCGCATGATGCTGACTTGGGC	1470

FIG. 5F

T416	1486	GAATAATGGGCAAGTGACATACACCATCTTTGGA.GAGTTTATTCT.AGGA	1533
m-PC	1471	AGTAATGGAAAAGTGTATACCGTATCAAGGACTCCCCCGTTTCTCACTT	1520
T416	1534	AGTTCCATAACTACATATGTAACCAATTGA...CCCATCTAATGGAGCCAT	1580
m-PC	1521	AGT..CATTATTGACTTTTGAAACAGGAGAAAGTCACTGCTCAGAGGTCACT	1568
T416	1581	...CTATGCCC...TCAGAAATCTTTGA..TC...ATGA.AGAAGTGAGTC	1618
m-PC	1569	GGACTATGAACACAGATGGCAGGCTTTGAGTTCAGGTGATAGCAGAG.GAC	1617
T416	1619	AGATCAC.TTTTGTGTAGAAAGCAAGAGATGGAGGAAGCCCGAAGCAACT	1667
m-PC	1618	AGAGGGCAACCCAGCTCGCATCCAG.CATCTCGGTGTGGGTAGCCCTCT	1666
T416	1668	GGTAAGC.....AATACCACAGTTGTG.CTCACC.....ATCATTGAC	1704
m-PC	1667	TGGATGCCCAATGATAATGCCCCAGAAAGTGATTACAGCCTGTGCTCAGTGAA	1716

FIG. 5G

T416	1705	GAATAATGACAACGTTCTGTGGTTATA.....GGGCC.....	1736
m-PC	1717	GGCAAAGCCACCCCTTTTCGGTGTCTTGTAATGCCTCCACGGGCCACCTTCT	1766
T416	1737	..TG..CATTGCGTA.....AT.AATACGGCAGAAATCACCATTCT	1771
m-PC	1767	GTTGCCCATTTGAGAAATCCACAGTGGCATGGATCCAGCAGGTACTGGTATAC	1816
T416	1772	..CCAAAGG.GGCTGAAAG....TGG.CTTT.CATGTCACAAGAATAAGG	1812
m-PC	1817	CACCAAAGGCTACCCACAGCCCCCTGGTCTTTTCCTTTTGTAAACAATCGTG	1866
T416	1813	GCAATTGACAGAGACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCATAGT	1862
m-PC	1867	GCTAGGGATGCAGACTCGGGGGCCAAATGGGGAACCTCTCTACAGCATTC	1916
T416	1863	AGCAGGTAATGAGGAGAAATATCTTCATAAATTGATCCACGATCATGTGACA	1912
m-PC	1917	AAGTGGGAATGATGCTCATCTCTT.TTTCCTCAGCC.CTTCCTTGGGGCA	1964

FIG. 5H

T416	1913	TCCAT..ACCAACGTTAGC.ATGGATTCTGTCCCTACACAG..AATGGG	1957
m-PC	1965	GCTATTCAATTAATGTCACCAATGCCAGCAGCCTCATCGGGAGTCAGTGGG	2014
T416	1958	AGCTGTCAGTTATCATTCAGGACAAAGGCAATCCTCAGCTACATACCAA	2007
m-PC	2015	ACCTGGGATAGTGGTAGAGGACCAGGGCAGCCCTCCTTGCAGACCCAA	2064
T416	2008	GTCCCTTCTGAAGTGCATGATCTTTGAATATGCAGAGTCGGTGACAAGTAC	2057
m-PC	2065	GTTTCATTGAAGGTCGTG...TTTG..TCACCAGTGT..GGACCACCTAA	2107
T416	2058	AGCAATGACTTCAGTAAGCCAGGCATCCTTGGATGTCTCCATGA.TAATA	2106
m-PC	2108	GGGATTCTGCTCA.TGAGCCCGGAGTTCT..GAGCACACCAGCACTGGCT	2154
T416	2107	ATTATTTCCCTTAGGAGCAATTGTGTCAGTGTGCTGGTTATTATGGTGCT	2156
m-PC	2155	TTGATCTGCCCTGGCTGTACTGCTGGCCATCTTTGGATTGCTCTTAGCCCT	2204

FIG. 5I

T416	2157	ATTTGCAACTAGGTGTAAACCGCGAGAGAAAGACACTAGATCCTATAACT	2206
m-PC	2205	GTTCGTGTCCATCTGCAGGACAGAGAGAAAGGATAATAGGGCCCTACAAC	2254
T416	2207	GCAGGGTGGCCGAATCAACTTACCAGCACCCAAAAGGCCATCCCGG	2256
m-PC	2255	GTCGAGAGCTGAGTCGTCAATACCGCCACCCAGCCCAAGAGGCCCCAGAAA	2304
T416	2257	CAGATTCACAAAGGGGACATCACATTGGTGCCTACCATAAATGGCACTCT	2306
m-PC	2305	CACATTCAGAAGGCAGATATCCACCTGGTGCCTGTGCT.TAGGGCCAC.	2352
T416	2307	GCCCATCAGATCTCATCA...CAGATCGTCTC.CATCTTCATCTCCTA..	2350
m-PC	2353	GAGAAATGAGA.CTGATGAAGTCAGGCCCATCTCACAAAGGATACCAGCAAGG	2401
T416	2351	..CCTTAGAAAGAGGCAGATGGG.....CAGCCGGCAGAGTCACAA	2390
m-PC	2402	AGACACTGATGGAGGCAGGCTGGGACTCTTGCCCTGGAGGCCCCCTTCCAC	2451

FIG. 5J



T416	2391	CAGTCACCAGTCACTCAACAGTTTGGTGACAAATCTCATCAAAACCACG...	2437
m-PC	2452	CTCACACCA.ACCCTATACAGGACCCCTGCGTAACCAAGGCAACCAGGGAG	2500
T416	2438	...TGCCAGA.....GAATTTCT.CATTAGAAC.TCACC...CACGCC	2472
m-PC	2501	AACTGGCAGAGAGCCAGGAGGTACTGCAGGACACCTTCAACTTCTCTTT	2550
T416	2473	ACTCCTGC..TGTTGA.GCAGGTCTCTC...AGCTTCT...TTCAATGC	2512
m-PC	2551	AACCATCCAGGCAGAGGAATGCCTCCCGGAGAACCTAAACCTTCCTGA	2600
T416	2513	TTCAACCAGGGGCAATA..TCAGCCAAGACCAAG..TTTTCGAGGAAACAA	2558
m-PC	2601	GTCCCCACCTGCTGTACGCGCAACCACTCTTAAGGCCCTCTGAAGGTGCCCTG	2650
T416	2559	ATATTCCAGGAGCTACAGATA.TGCCCTTCAAGACATGACAAAATTAGC	2607
m-PC	2651	GTAGCCCCATAGCGAGGGCGGACTGGAGACCAAGACAAGGAGGA...GGC	2696

FIG. 5K

T416	2608	TTGAAAAGACAGTGGCCGTGGTGACAGTGAGGC..AGGAGACAG.TGATTA	2654
m-PC	2697	CCCACAGAGCCCACACAGCGTCCCTCTGCAACCCCTAAGACGACAGCGGAATT	2746
T416	2655	TGATTTGGGCGAGATTCTCCAATA.GATAGGCTGCTGGTGAAGGATTC	2703
m-PC	2747	TCAAT..GGCAAAGTGTCTCCTAGAGGAGAGTCCGGTCTCATCAGATTC	2794
T416	2704	..AGCGACCTGTTT...CTCACAGATGGAAGAATTCCAGCAGCTATGAGA	2748
m-PC	2795	TGAGGAGCCTGGTTAGGCTCTCTG.TGGCTGCTTTTGCGGA...ACGGAA	2840
T416	2749	CTCTGCACGGAGGAG..TGCAGGGTCCCTGGGACACTCTGACCAGTGCTGG	2796
m-PC	2841	CCCCG..TGGAGGAGCCTGCTGGGGACT..CTCCTCCTGTCCAGCAAATC	2886
T416	2797	ATGCCACCACTGCCCTCAC...CGTCTTCTGATTATAGGAGTAACATGT	2842
m-PC	2887	TCCCAGCTGCTGTCTTGTCTGCACCAGGGCCAAATTCCAGCCCCAAACCAA	2936

FIG. 5L

T416	2843	TCATTCCAGGGGAAGAATTCCCAACGCAACCCAGCAGCAGCATC.....	2887
m-PC	2937	CCA..CCGAGGAAATAAATACTTGGCCAAGCCCGCGGCAGCAGCAGGGG	2984
T416	2888	.CACATCAGAGTC.TTGAGGATGACGCTCAGCCTGCAGATTCCGGTGAAA	2935
m-PC	2985	TACCATCCAGACACACAGAGGGCCTTG.TAGGCCTCAAGCCT.AGTGGCCA	3032
T416	2936	AGAAGAAGAGTTTTCCACCTTTGGAAAGGACTCCCCAAACGATGAGGAC	2985
m-PC	3033	AGCAGAA.....CCTGACCTGGAAGAAGGC.CCCCGAGCCCGGAGGA.	3074
T416	2986	ACTGGGGATACCAGCACATC.ATCTCTGCTCTCGGAAATGAGCAGTGTGT	3034
m-PC	3075	...GGACCTTCTGTAAAGCGACTTCTAGAAGAAGAGCTGTCGAGCCTGT	3121
T416	3035	TCCAGCGTCTCTTACCGCCTTCCCTGGACA..CCTATTCTGAATGCAGTG	3082
m-PC	3122	TGGACCCCTAATACAGGTCTAGCCCTGGACAAGCTGAGTCCGCCCTGACCCA	3171

FIG. 5M

T416	3083	AGGTGGATCG.GTCCAACCTCCCTGGAGCGCAGGAAGGACCCTTGCCAGC	3131
m-PC	3172	GCCTGGATGGCGAGATTGTTCATTTGCCCTCA.....CCACCAATTATCGA	3216
T416	3132	CAAAACTGTGGGTTACCCACAGGGGTAGCGGCATGGGCAGCCAGTACGC	3181
m-PC	3217	GACAACT.TGTCTTCCCCCGATGCTACAACATCAGAGGAACCGAGAAC..	3263
T416	3182	ATTTTCAAAAATCCACCACTGTGGGCGGCCACTTGGAACCTCACTCC	3231
m-PC	3264	.CTTCCAGACATTTCGGCAAGACAGTTGGACCGGGAC.CCGAGCTGAGCCC	3311
T416	3232	AGTGTGCAGCCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGATCCCT..	3279
m-PC	3312	AACAGGCACGCGCCTGGCCAGCACCTTTCGTCTCGGAGATGAGCTCTCTGC	3361
T416	3280	..GAAA..ATTATGAGGAAGATGATTTTGACAATG..TGCT.CAACCACC	3322
m-PC	3362	TGGAAATGTTGTTGGGCGAGCACACGGTACCACTGGAAGCTGCGTCCGCG	3411

FIG. 5N

T416	3323	TCAATGATGGGAAACACGAACTCATGGATG....CCAGT...GA.....	3359
m-PC	3412	GCTTTGCGGAGGCTCTCGGTGTGCGGAGGACCCCTCAGTCTAGACCTAGC	3461
T416	3360	....ACTGGTGGCAGAGATTAAACA..ACTGCTT..CAAGATGTCCGC.C	3400
m-PC	3462	CACCAGTGGGGCTTCAGCTTCAGAAAGCACAGGGTAGAAAGAGCAGCTG	3511
T416	3401	AGAGC.....	3405
m-PC	3512	AGAGCAGACTTGGCTGTGGCAGGAATCTA	3540

FIG. 50

m-PC	1	MMLLLPFLGLLPGSYLFISGDCQEVATVMVKFQVTEEVPSTGIGKLS	50
T416	1	.MHQMNAKMHFRFVFALLIVSFN.HDVLGKNLKYRIYEEQRVGSVIARLS	48
m-PC	51	QELR..VEERRGKAGDAFQILQLPQALPVQMNSDGLLSTSSRLDREKLC	98
T416	49	EDVADVLLKLPNPSTVRFAMQRGNSPLLVVNEDNGEISIGATIDREQLC	98
m-PC	99	RQEDPCLVSFDV..LATGASALIHVEIQVLDINDHQPFQPKDEQELEISE	146
T416	99	QKNLNCSEFDVITLPTTEHLQLFHIEVEVLDINDNSPQFSRSLPIEISE	148
m-PC	147	SASLHTRIPLDRALDQDTGPNLSLYSLSPEHFAFDVIVGPDETKHAEL	196
T416	149	SAAVGTRIPLDSAFDPDVGENSLHTYSLSANDFFNIEVTRTRTDGAKYAE	198
m-PC	197	VVKELDRHLSYFDLVLTAIDNGNPPKSGISVVKVNLDSNDNSPVFAE	246
T416	199	IVVRELDRELKSSYELQLTASDMGVQPQRSGSSILKISISDSNDNSPAFEQ	248

FIG. 6A

m-PC	247	SSLALEIPEDTVPGTLLINLTATDPDQGPNGEVEFFGKHVSPEVMNTFG	296
T416	249	QSYIIQLENSPVGTLTLLDNATDPDEGANGKIVYSFSSHVSPKIMETFK	298
m-PC	297	IDAKTGQIILRQALDYEKNPAYEVDVQARDLGPNSIPGHCKVLIKVLDVN	346
T416	299	IDSERGHLTLFKQVDYEITKSYEIDVQAQDLGPNSIPAHCKI I I KVVVDVN	348
m-PC	347	DNAPSILITWAS...QTSLVSEDLPRDSFIALVSANDLDSGNNGLVHCW	392
T416	349	DNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKDGLNGEIVCK	398
m-PC	393	LNQELGHFRLKRTNGNTYMLLTNATLDREQWPIYTLTVFAQDQGPQLSA	442
T416	399	LHGH.GHFKLQKTYENNYLLTNATLDREKRSEYSLTVIAEDRGTPSLST	447
m-PC	443	EKELQIQVSDVNDNAPVFEKSRYEVSSTWENNPPSLHLITLKAHDADLGSN	492
T416	448	VKHFTVQINDINDNPPHFQRSRYEFVISENNSPGAYITTVTATDPDLGEN	497

FIG. 6B







m-PC	982	GNKYLAKPGSSRGTI	PDTEGLVGL.KPSGQAEPDLEE	PPSPPEEDLSVK	1030
T416	964	HQLEDDAQPADSGEKK	SFSTFGKDSPNDEDTGDTSTSSLLSEMSSVFQ	1013	
m-PC	1031	RLLEEEL...	SSLLDPNTGLALDKLSPDP	PAWMARLSPLTTNYRDNLSS	1077
T416	1014	RLPPSLD	TYSECSEVDRSNSLERRKGPLPAKTVGYPQGVAAWAASTHFQ	1063	
m-PC	1078	PDATTEEPRTFQTFGKTVGPGPELSPTGTRLASTFVSEMSSLLEMLLGQ	1127		
T416	1064	NPTNCGPPLGTHS...	SVQPSSKWLPAEMEEIPENYEEDDFDNVLNHLND	1110	
m-PC	1128	HTVPVEAAASAAALRRLSVCGRTL	SLDLATSGASASEAQGRKKAESRLGCCGRNL	1180	
T416	1111	GKHELMDASELVAEINKLLQDVRQS	.....	1135	

FIG. 6E

GAAGTGGGAT	GTGCAAAAGC	GCCGGCTGGA	AATCCCGGCT	GTGTCTCCGT	CAACTCTTTA	60
CGCAACAGAG	GTCTCCCCCT	GCCCTTGGTT	TCTACCGGGC	CGCCTGCTCC	CACTCGGCGA	120
AAAAAATTAC	ACAACAGCAG	CCGCGGCG	ATG ACG	TGG AGG	GCT GCC	172
	Met Thr	Trp Arg	Ala Ala	Ala Ser		8
ACG TGC	GCG CTC	CTG ATT	CTG CTG	TGG GCG	CTG ACC	GAA GGT
Thr Cys	Ala Ala	Leu Leu	Ile Leu	Trp Ala	Leu Thr	Glu Gly
						24
GAT CTG	AAA GTA	GAG ATG	GCA GGG	GGG ACT	CAG ATC	ACA CCC
Asp Leu	Lys Val	Glu Met	Met Ala	Gly Gly	Thr Gln	Ile Thr
						Pro Leu
						40
AAT GAC	AAT GTC	ACC ATA	TTC TGC	AAT ATC	TTT TAT	TCC CAA
Asn Asp	Asn Val	Thr Ile	Phe Thr	Cys Asn	Ile Phe	Tyr Ser
						Gln Pro
						Leu
						56
AAC ATC	ACG TCT	ATG GGT	ATC ACC	TGG TTT	TGG AAG	AGT CTG
Asn Ile	Thr Ser	Met Gly	Ile Thr	Trp Phe	Trp Lys	Ser Leu
						Thr Phe
						72
GAC AAA	GAA GTC	AAA GTC	TTT GAA	TTT TTT	GGA GAT	CAC CAA
Asp Lys	Glu Val	Val Lys	Val Phe	Phe Phe	Gly Asp	His Gln
						Glu Ala
						88
TTC CGA	CCT GGA	GCC ATT	GTG TCT	CCA TGG	AGG CTG	AAG AGT
Phe Arg	Pro Gly	Ala Ile	Val Ser	Pro Trp	Arg Leu	Lys Ser
						Gly Asp
						104
GCC TCA	CTG CGG	CTG CCT	GGA ATC	CAG CTG	GAG GAA	GCA GAG
Ala Ser	Leu Arg	Leu Pro	Gly Ile	Gln Leu	Glu Glu	Ala Gly
						Tyr
						120
						508

Fig. 7A

CGA TGT GAG GTG GTG GTC ACC CCT CTG AAG GCA CAG GGA ACA GTC CAG	556
Arg Cys Glu Val Val Val Thr Pro Leu Lys Ala Gln Gly Thr Val Gln	136
CTT GAA GTT GTG GCT TCC CCA GCC AGC AGA TTG TTG CTG GAT CAA GTG	604
Leu Glu Val Val Ala Ser Pro Ala Ser Arg Leu Leu Asp Gln Val	152
GGC ATG AAA GAG AAT GAA GAC AAA TAT ATG TGT GAG TCA AGT GGG TTC	652
Gly Met Lys Glu Asn Glu Asp Lys Tyr Met Cys Glu Ser Ser Gly Phe	168
TAC CCA GAG GCT ATT AAT ATA ACA TGG GAG AAG CAG ACC CAG AAG TTT	700
Tyr Pro Glu Ala Ile Asn Ile Thr Trp Glu Lys Gln Thr Gln Lys Phe	184
CCC CAT CCC ATA GAG ATT TCT GAG GAT GTC ATC ACT GGT CCC ACC ATC	748
Pro His Pro Ile Glu Ile Ser Glu Asp Val Ile Thr Gly Pro Thr Ile	200
AAG AAT ATG GAT GGC ACA TTT AAT GTC ACT AGC TGC TTG AAG CTG AAC	796
Lys Asn Met Asp Gly Thr Phe Asn Val Thr Ser Cys Leu Lys Leu Asn	216
TCC TCT CAG GAA GAC CCT GGG ACT GTC TAC CAG TGT GTG GTA CGG CAT	844
Ser Ser Gln Glu Asp Pro Gly Thr Val Tyr Gln Cys Val Val Arg His	232
GCG TCC TTG CAT ACC CCC TTG AGG AGC AAC TTT ACC CTG ACT GCT GCT	892
Ala Ser Leu His Thr Pro Leu Arg Ser Asn Phe Thr Leu Thr Ala Ala	248
CGG CAC AGT CTT TCT GAA ACT GAG AAG ACA GAT AAT TTT TCC ATT CAT	940
Arg His Ser Leu Ser Glu Thr Glu Lys Thr Asp Asn Phe Ser Ile His	264

Fig. 7B

TGG TGG CCT ATT TCA TTC ATT GGT GTT GGA CTG GTT TTA TTA ATT GTT	988
Trp Trp Pro Ile Ser Phe Ile Gly Val Gly Leu Val Leu Leu Ile Val	280
TTG ATT CCT TGG AAA AAG GTA AGG GGC TCC AAA GCA AAG TTC AGC CCT	1036
Leu Ile Pro Trp Lys Lys Val Arg Gly Ser Lys Ala Lys Phe Ser Pro	296
GTG TCT TGG GCT AGT AAA AAG CTT TTA GAG CAG CTG CTG CCA ACC TTA	1084
Val Ser Trp Ala Ser Lys Lys Leu Leu Leu Gln Leu Pro Thr Leu	312
CAA GCC TCA AGG GAC AGG CCT GCT GGA AAG GAC TTT GTC AGT CCC TCT	1132
Gln Ala Ser Arg Asp Arg Pro Ala Gly Lys Asp Phe Val Ser Pro Ser	328
TCA CCA TCA GGT GTT GGG AAT GTT GGC TGT GTT CCA ATC CAG TTT CCT	1180
Ser Pro Ser Gly Val Gly Val Gly Asn Val Gly Cys Val Pro Ile Gln Phe Pro	344
ATC ACA GAG GAC CTA GCT GTC ACA TAC CAT CTG ACC TCT GTA TGG TGG	1228
Ile Thr Glu Asp Leu Ala Val Thr Tyr His Leu Thr Ser Val Trp Trp	360
TTT GTG ACT CTG GGG TGATGTGTG TAAAGCCTCC CTCTCTTTCT CCATACTAAA	1283
Phe Val Thr Leu Gly	365
CAAGTATTAT ATCTCTGTGA ATGAACCAGA CTTTAGTGTT CAGACCAGGC CCTGAACATAT	1343
GTGTGGACTG CTTGTTTTTC TCACACATTT AGAAACTATG GCTTAGAGAG GGAATTCCT	1403
CATATTTTAT CTGATCAATA ACTGACCACC AGATCTCACT AGTTTGACTA AGAATTTCTA	1463
ACCCTCACTA GGTATTTCTA AACTAAAACA TGTTTCTAAA CATTTTATC CCTGACTATG	1523

Fig. 7C

GCCCAATAG	TAAATAAAC	AGCTCAAGCT	TTAGAGGCC	AAGAGACCTA	TGTAAATGTG	1583
TTGGTTAAAA	TAGTTTTAGA	TAATAAAAGG	GCCCTCAATT	ATTTATGGC	CTGTCAAAGGC	1643
AAAATCTGCA	CAACAGCCAG	TACATCTCAT	TATAAATAAT	TTAGGAGAAG	TGGAATAATC	1703
AGTCAATTAA	GAAAAATGGC	CCTTTATCTA	AAGTTGCCA	TTTAGATTCA	CGGGACTTAT	1763
TCCTGTTGGA	TCTAGGCCAT	GAGAAAACCTG	GATAAAAAGT	GGTTTCAAA	TGTTTCTTGT	1823
GGTATTTGTG	ACTGTTGTCA	TATTTCTTGC	CTTCTCTGG	TTCTGATATT	CAGGTGCTAT	1883
TGAGAGAGGA	GGAAGGAAGA	AACTAGTCAG	GCAGGCAGTT	AGGGTGGCC	CTCAGTCAAA	1943
TTCCCTTCAA	CAAAAGAACA	GCCTGAAAA	TCAAACCTGCA	GATAAGGAA	CTTGACAGG	2003
GGGCTTGCC	TAAACATGC	CCACAGCCAC	ATACATTAAA	ACAAGGCTAC	ACAGGAGACT	2063
TGCCTAGACA	TGCTCACAAT	AGAAAATTCC	ATCCCCTGAC	ACATGCACAG	TAAGGGGAAC	2123
AAAGCCACAT	GGAGTAACTC	AAGCTAAGGG	CTTGCATGCA	CACTACGAGG	ATGGGGTGGA	2183
GCTACCAGAA	ATGTGTGCCT	TATGCCCTTG	TATTCAGCTG	TGAAATGGCA	ACCCCTCTTT	2243
GGCCCCCCTC	TCTGCAGTGG	AGTGCTTTCT	TCTTTTGCTT	ATTAAACTTT	CACTTCAACT	2303
TCAAAAAAAA	AAAAA	AAAAA				2330

Fig. 7D

GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGC	2246
GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGC	121136
CCAAAAGAGG	GTTGCCATTT	CACAGCTGAA	TACAAAGGCA	TAAAGGCACAC	ATTTCTGGTA	2186
CCAAAAGAGG	GTTGCCATTT	CACAGCTGAA	TACAAAGGCA	TAAAGGCACAC	ATTTCTGGTA	121196
GCTCCACCCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	2126
GCTCCACCCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	121256
TTGTTCCCCCT	TACTGTGCAT	GTGTCAGGGG	ATGGAATTTT	CTATTGTGAG	CATGTCTAGG	2066
TTGTTCCCCCT	TACTGTGCAT	GTGTCAGGGG	ATGGAATTTT	CTATTGTGAG	CATGTCTAGG	121316
CAAGTCTCCT	GTGTAGCCCTT	GTTTAAATGT	ATGTGGCTGT	GGGCATGTTT	TAGGCAAGCC	2006
CAAGTCTCCT	GTGTAGCCCTT	GTTTAAATGT	ATGTGGCTGT	GGGCATGTTT	TAGGCAAGCC	121376
CCCCGTGTACA	AGTTCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTTGAAGG	1946
CCCCGTGTACA	AGTTCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTTGAAGG	121436

Fig. 9A

AATTGACTG	AGGGCCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCTT	CCTCCTCTCT	1886
AATTGACTG	AGGGCCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCTT	CCTCCTCTCT	121496
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGGCAAGAAA	TATGACAACA	GTCACAAAATA	1826
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGGCAAGAAA	TATGACAACA	GTCACAAAATA	121556
CCACAAGAAA	CATTGAAAA	CCACTTTTA	TCCAGTTTC	TCATGGCCTA	GATCCAACAG	1766
CCACAAGAAA	CATTGAAAA	CCACTTTTA	TCCAGTTTC	TCATGGCCTA	GATCCAACAG	121616
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAATTGA	1706
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAATTGA	121676
CTGATTATTC	CACCTCTCCT	AAATTATTTA	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	1646
CTGATTATTC	CACCTCTCCT	AAATTATTTA	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	121736
TTGCCCTTGAC	AGGCCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	1586
TTGCCCTTGAC	AGGCCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	121796

Fig. 9B



AACACATTTA	CATAGGTCTC	TTGGGCCCTCT	AAAGCTTGAG	CTGTTTATT	TACTATTGG	1526
AACACATTTA	CATAGGTCTC	TTGGGCCCTCT	AAAGCTTGAG	CTGTTTATT	TACTATTGG	121856
GCCATAGTCA	GGGATAAAAA	TGTTTAGAAA	CATGTTTAG	TTTAGAAAATA	CCTAGTGAGG	1466
GCCATAGTCA	GGGATAAAAA	TGTTTAGAAA	CATGTTTAG	TTTAGAAAATA	CCTAGTGAGG	121916
GTTAGAAATT	CTTAGTCAAA	CTAGTGAGAT	CTGGTGGTCA	GTTATTGATC	AGATAAAATA	1406
GTTAGAAATT	CTTAGTCAAA	CTAGTGAGAT	CTGGTGGTCA	GTTATTGATC	AGATAAAATA	121976
TGAGGAATTC	CCCTCTCTAA	GCCATAGTTT	CTAAATGTGT	GAGAAAAACA	AGCAGTCCAC	1346
TGAGGAATTC	CCCTCTCTAA	GCCATAGTTT	CTAAATGTGT	GAGAAAAACA	AGCAGTCCAC	122036
ACATAGTTCA	GGGCCTGGTC	TGAACACTAA	AGTCTGGTTC	ATTCACAGAG	ATATAATACT	1286
ACATAGTTCA	GGGCCTGGTC	TGAACACTAA	AGTCTGGTTC	ATTCACAGAG	ATATAATACT	122096
TGTTTAGTAT	GGAGAAAGAG	AGGAGGCTT	TACAACACAT	CACCCCAGAG	TCACAAACCA	1226
TGTTTAGTAT	GGAGAAAGAG	AGGAGGCTT	TACAACACAT	CACCCCAGAG	TCACAAACCA	122156

Fig. 9C

CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	1166
CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	122216
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAGT	CCTTTCACG	1106
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAGT	CCTTTCACG	122276
AGGCCGTGCC	CTTGAGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	1046
AGGCCGTGCC	CTTGAGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	122336
CCAAGACACA	GGGCTGAACT	TTGCTTTGGA	GCCCCCTTACC	TTTTTCCAAG	GAATCAAAAC	986
CCAAGACACA	GGGCTGAACT	TTGCTTTGGA	GCCCCCTTACC	TTTTTCCAAG	GAATCAAAAC	122396
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGGAATAATT	926
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGGAATAATT	122456
ATCTGTCTTC	TCAGTTTCAG	AA				904
ATCTGTCTTC	TCAGTTTCTG	CA				122478

Fig. 9D

	M V		2
GGCCCCGGCAGCTGCGGCTCGGGATCCGTCGAGGGAGGCCGAGCTTGCCAAAGCTGGCGCCAGCGGGGTC	ATG	GTG	77
P G A R G G G A L A R A A G R G L L A L	A	L	22
CCC GGC GCC CGC GGC GGC GCA CTG GCG CGG GCT GCC GGC CGG GGC CTC CTG GCT TTG	CTG	TTG	137
L L A V S A P L R L Q A E E L G D G C G	C	G	42
CTG CTC GCG GTC TCC GCC CCG CTC CGG CTG CAG GCG GAG GAG CTG GGT GAT GGC TGT GGA	TGT	GGA	197
H L V T Y Q D S G T M T S K N Y P G T Y	T	Y	62
CAC CTA GTG ACT TAT CAG GAT AGT GGC ACA ATG ACA TCT AAG AAT TAT CCC GGC ACC TAC	ACC	TAC	257
P N H T V C E K T I T V P K G K R L I L	I	L	82
CCC AAT CAC ACT GTT TGC GAA AAG ACA ATT ACA GTA CCA AAG GGC AAA AGA CTG ATT CTG	ATT	CTG	317
R L G D L D I E S Q T C A S D Y L L F T	F	T	102
AGG TTG GGA GAT TTG GAT ATC GAA TCC CAG ACC TGT GCT TCT GAC TAT CTT CTC TTC ACC	CTC	ACC	377
S S S D Q Y G P Y C G S M T V P K E L L	L	L	122
AGC TCT TCA GAT CAA TAT GGT CCA TAC TGT GGA AGT ATG ACT GTT CCC AAA GAA CTC TTG	CTC	TTG	437
L N T S E V T V R F E S G S H I S G R G	R	G	142
TTG AAC ACA AGT GAA GTA ACC GTC CGC TTT GAG AGT GGA TCC CAC ATT TCT GGC CGG GGT	CGG	GGT	497

Fig. 10A

F	L	L	T	Y	A	S	S	D	H	P	D	L	I	T	C	L	E	R	A	162
TTT	TTG	CTG	ACC	TAT	GCG	AGC	AGC	GAC	CAT	CCA	GAT	TTA	ATA	ACA	TGT	TTG	GAA	CGA	GCT	557
S	H	Y	L	K	T	E	Y	S	K	F	C	P	A	G	C	R	D	V	A	182
AGC	CAT	TAT	TTG	AAG	ACA	GAA	TAC	AGC	AAA	TTC	TGC	CCA	GCT	GGT	TGT	AGA	GAC	GTA	GCA	617
G	D	I	S	G	N	M	V	D	G	Y	R	D	T	S	L	L	C	K	A	202
GGA	GAC	ATT	TCT	GGG	AAT	ATG	GTA	GAT	GGA	TAT	AGA	GAT	ACC	TCT	TTA	TTG	TGC	AAA	GCT	677
A	I	H	A	G	I	I	A	D	E	L	G	G	Q	I	S	V	L	Q	R	222
GCC	ATC	CAT	GCA	GGA	ATA	ATT	GCT	GAT	GAA	CTA	GGT	GGC	CAG	ATC	AGT	GTG	CTT	CAG	CGC	737
K	G	I	S	R	Y	E	G	I	L	A	N	G	V	L	S	R	D	G	S	242
AAA	GGG	ATC	AGT	CGA	TAT	GAA	GGG	ATT	CTG	GCC	AAT	GGT	GTT	CTT	TCG	AGG	GAT	GGT	TCC	797
L	S	D	K	R	F	L	F	T	S	N	G	C	S	R	S	L	S	F	E	262
CTG	TCA	GAC	AAG	CGA	TTT	CTG	TTT	ACC	TCC	AAT	GGT	TGC	AGC	AGA	TCC	TTG	AGT	TTT	GAA	857
P	D	G	Q	I	R	A	S	S	S	W	Q	S	V	N	E	S	G	D	Q	282
CCT	GAC	GGG	CAA	ATC	AGA	GCT	TCT	TCC	TCA	TGG	CAG	TCG	GTC	AAT	GAG	AGT	GGA	GAC	CAA	917
V	H	W	S	P	G	Q	A	R	L	Q	D	Q	G	P	S	W	A	S	G	302
GTT	CAC	TGG	TCT	CCT	GGC	CAA	GCC	CGA	CTT	CAG	GAC	CAA	GGC	CCA	TCA	TGG	GCT	TCG	GGC	977

Fig. 10B

D	S	S	N	N	H	K	P	R	E	W	L	E	I	D	L	G	E	K	K	322
GAC	AGT	AGC	AAC	AAC	CAC	AAA	CCA	CGA	GAG	TGG	CTG	GAG	ATC	GAT	TTG	GGG	GAG	AAA	AAG	1037
K	I	T	G	I	R	T	T	G	S	T	Q	S	N	F	N	F	Y	V	K	342
AAA	ATA	ACA	GGA	ATT	AGG	ACC	ACA	GGA	TCT	ACA	CAG	TCG	AAC	TTC	AAC	TTT	TAT	GTT	AAG	1097
S	F	V	M	N	F	K	N	N	N	S	K	W	K	T	Y	K	G	I	V	362
AGT	TTT	GTG	ATG	AAC	TTC	AAA	AAC	AAT	AAT	TCT	AAG	TGG	AAG	ACC	TAT	AAA	GGA	ATT	GTG	1157
N	N	E	E	K	V	F	Q	G	N	S	N	F	R	D	P	V	Q	N	N	382
AAT	AAT	GAA	GAA	AAG	GTG	TTT	CAG	GGT	AAC	TCT	AAC	TTT	CGG	GAC	CCA	GTG	CAA	AAC	AAT	1217
F	I	P	P	I	V	A	R	Y	V	R	V	V	P	Q	T	W	H	Q	R	402
TTC	ATC	CCT	CCC	ATC	GTG	GCC	AGA	TAT	GTG	CGG	GTT	GTC	CCC	CAG	ACA	TGG	CAC	CAG	AGG	1277
I	A	L	K	V	E	L	I	G	C	Q	I	T	Q	G	N	D	S	L	V	422
ATA	GCC	TTG	AAG	GTG	GAG	CTC	ATT	GGT	TGC	CAG	ATT	ACA	CAA	GGT	AAT	GAT	TCA	TTG	GTG	1337
W	R	K	T	S	Q	S	T	S	V	S	T	K	K	E	D	E	T	I	T	442
TGG	CGC	AAG	ACA	AGT	CAA	AGC	ACC	AGT	GTT	TCA	ACT	AAG	AAA	GAA	GAT	GAG	ACA	ATC	ACA	1397
R	P	I	P	S	E	E	T	S	T	G	I	N	I	T	T	V	A	I	P	462
AGG	CCC	ATC	CCC	TCG	GAA	GAA	ACA	TCC	ACA	GGA	ATA	AAC	ATT	ACA	ACG	GTG	GCT	ATT	CCA	1457

Fig. 10C

L	V	L	L	L	V	V	L	V	F	A	G	M	G	I	F	A	A	F	R	K	482
TTG	GTG	CTC	CTT	GTT	GTC	CTG	CTG	GTG	TTT	GCT	GGA	ATG	GGG	ATC	TTT	GCA	GCC	TTT	AGA	AAG	1517
K	K	K	K	G	S	P	Y	G	S	A	E	A	Q	K	T	D	C	W	K	502	
AAG	AAG	AAG	AAA	GGA	AGT	CCG	TAT	GGA	TCA	GCA	GAG	GCT	CAG	AAA	ACA	GAC	TGT	TGG	AAG	1577	
Q	I	K	Y	P	F	A	R	H	Q	S	A	E	F	T	I	S	Y	D	N	522	
CAG	ATT	AAA	TAT	CCC	TTT	GCC	AGA	CAT	CAG	TCA	GCT	GAG	TTT	ACC	ATC	AGC	TAT	GAT	AAT	1637	
E	K	E	M	T	Q	K	L	D	L	I	T	S	D	M	A	D	Y	Q	Q	542	
GAG	AAG	GAG	ATG	ACA	CAA	AAG	TTA	GAT	CTC	ATC	ACA	AGT	GAT	ATG	GCA	GAT	TAC	CAG	CAG	1697	
P	L	M	I	G	T	G	T	V	T	R	K	G	S	T	F	R	P	M	D	562	
CCC	CTC	ATG	ATT	GGC	ACC	GGG	ACA	GTC	ACG	AGG	AAG	GGC	TCC	ACC	TTC	CGG	CCC	ATG	GAC	1757	
T	D	A	E	E	A	G	V	S	T	D	A	G	G	H	Y	D	C	P	Q	582	
ACG	GAT	GCC	GAG	GAG	GCA	GGG	GTG	AGC	ACC	GAT	GCC	GGC	GGC	CAC	TAT	GAC	TGC	CCG	CAG	1817	
R	A	G	R	H	E	Y	A	L	P	L	A	P	P	E	P	E	Y	A	T	602	
CGG	GCC	GGC	CGC	CAC	GAG	TAC	GCG	CTG	CCC	CTG	GCG	CCC	CGG	GAG	CCC	GAG	TAC	GCC	ACG	1877	
P	I	V	E	R	H	V	L	R	A	H	T	F	S	A	Q	S	G	Y	R	622	
CCC	ATC	GTG	GAG	CGG	CAC	GTG	CTG	CGC	GCC	CAC	ACG	TTC	TCT	GCG	CAG	AGC	GGC	TAC	CGC	1937	

Fig. 10D

V P G P Q P G H K H S L S S G G F S P V 642  
GTC CCA GGG CCC CAG CCC GGC CAC AAA CAC TCC CTC TCC TCG GGC GGC TTC TCC CCC GTA 1997

A G V G A Q D G D Y Q R P H S A Q P A D 662  
GCG GGT GTG GGC GCC CAG GAC GGA GAC TAT CAA AGG CCA CAC AGC GCA CAG CCT GCG GAC 2057

R G Y D R P K A V S A L A T E S G H P D 682  
AGG GGC TAC GAC CGG CCC AAA GCT GTC AGC GCC CTC GCC ACC GAA AGC GGA CAC CCT GAC 2117

S Q K P P T H P G T S D S Y S A P R D C 702  
TCT CAG AAG CCC CCA ACG CAT CCC GGG ACG AGT GAC AGC TAT TCT GCC CCC AGA GAC TGC 2177

L T P L N Q T A M T A L L \* 715  
CTC ACA CCC CTC AAC CAG ACG GCC ATG ACT GCC CTT TTG TGA 2219

ACACAATGTGAAAGAAGCCTGCTGTGGTACTGAGCGTCGGGCTGTCAAGGCACCTGGAAGAAGGAGCCTGCTGGTCC 2298  
AGAGTGTGCGTGTATCGGTGTGTGTACACTTGCATGTGTGTGTGTGATCCAGTAGGATCCTAGAGACAACCTGTC 2377  
ATACTGTTTACAAAATTGTGCAGCTGGTTTCGTGCTGACCCCTTAGGGTCCGTCTGTTGGGTTTGTGGGCTAGAAAAA 2456  
TGAAAAATTTTAGATGGCGTTTTCATTCCTCTGACTGATATTGAGCTGCTTTGGTGTAAAGGTGTAATGTGTACAGAG 2535  
TTGTATTTAACAATAATAAAGTAACCTTAAGTTTGCCTCTATCAGATTTTAGTTCTGCACAGAGGTTAAGTGGGAAAATG 2614  
CAGCTGTTGCCAAAATGTATATAAATAGTATGTTTCATTTTTCAGTATATATCTGATACCTGTGTAGCAGCAGTCTG 2693  
CTTAAACCTAGTCTTGTGTTATTGAGTCATTTCCCTCTCCTTTGATAACTAGAACTGAAAGCATTTTAAACATTCTTCT 2772  
CCTGGAAGAAATGAATTACTTGAAGCATGAAAGACACACAGGCTGTTGTTTATTAGCAATTATGACTGTAGATTTA 2851

Fig. 10E

```

AAAACAAAGAAACAAACACCTCAGCAGCTGCCCGTTTCCTTAGTCTCCACTTCAGAGGGGATCGAAGAGGTCGG 2930
CCCAGCTCCGGTGACCATGAAGGTGGCACAGGAATTACAGTGTGAATGGCTGTGTCTCAGATGTTTTTCGTACCTCAGATTA 3009
AAAATATTGCTGAGGTCAGACGCCACAATTTTCATGACTTTCTTCAGAAAGTAGCACATTTTCGTGACTTCCGCTGTCCT 3088
CTGAAAAACAAAGTTATTGGAAACATGTTCAATGCAAAAGTGATTCTGACCAAGTCTAAATCGAGCTTTTCTACTGACAT 3167
GAAACTGTTGGAAACTGATCTCATTTTATAAGAAATGATTTTCCCTCAAGGAGCGCTCTGTAATTCAGAACAGTCCA 3246
GACATCAGCTGTACCTCATGCTCAGTAGTTTATTGAGTTTCTTTGTGAGTTAACTATGGGAGATTTAACCTCTTT 3325
TGCCAAAGAGGGAAGTGTGTGTTTTTAATAGAAAATATGGACCAAAAATTTTTTCCCTGAAGAATGTATTATAA 3404
CCCTATTGTGTGGTTATTACATCCTGTGAAATGTATATATGTTAAAATAATGGGGGTGCTGGAAGGTCATGGCAGACT 3483
AGCTGCTGGTTAGTGTGGAGGGGAAGTGGTTTACTTTGTAGAGTTTACATGGTTTTATGCGCACACTAATTGTAATAA 3562
CTATGCCAAACCAATAAAAAAATAAAAAA

```

Fig. 10F



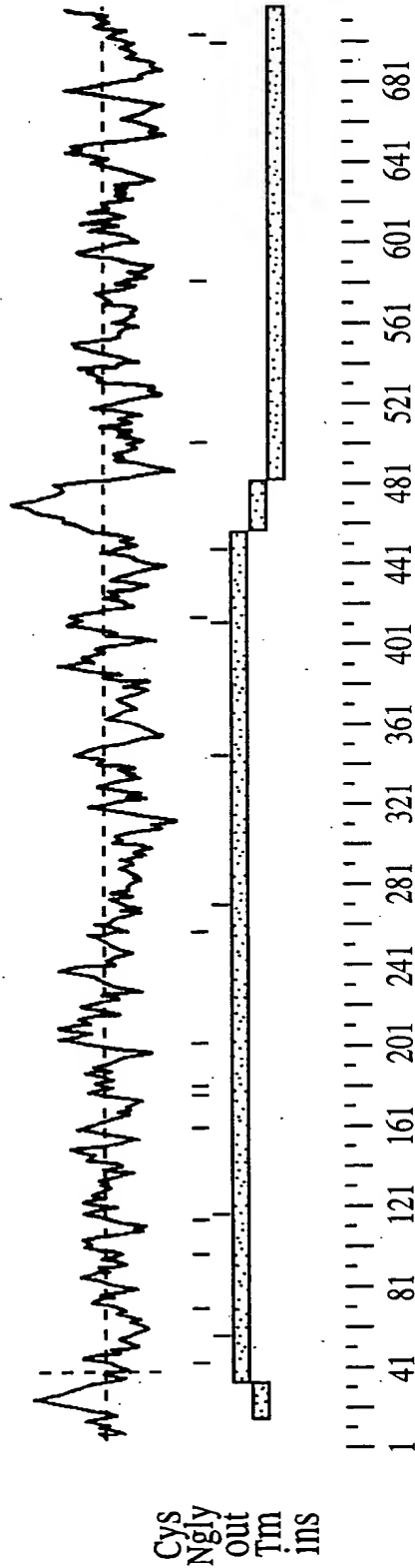


FIG. 10G

# Sequence

GTGGTCGCGCGGAGGTGAGACTGTGAAGAAGAAAGCTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGC	79
CCCTGCCTGCCACACCAAGCATTAGGCCACCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAG	158
<div>M N W H M I I S G L I V V</div> <div>GCCCCTGCAGCTCCTTCATC ATG AAC TGG CAC ATG ATC TCT GGG CTT ATT GTG GTA GTG</div>	14 220
<div>L K V V G M T L F L L Y F P Q I F N K S</div> <div>CTT AAA GTT GTT GGA ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT</div>	34 280
<div>N D G F T T T R S Y G T V S Q I F G S S</div> <div>AAC GAT GGT TTC ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT</div>	54 340
<div>S P S P N G F I T T R S Y G T V C P K D</div> <div>TCC CCA AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC</div>	62/361 74 400
<div>W E F Y Q A R C F F L S T S E S S W N E</div> <div>TGG GAA TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA</div>	94 460
<div>S R D F C K G K G S T L A I V N T P E K</div> <div>AGC AGG GAC TTT TGC AAA GGA AAA GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA</div>	114 520
<div>L K F L Q D I T D A E K Y F I G L I Y H</div> <div>CTG AAG TTT CTT CAG GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT</div>	134 580

Fig. 11A

R E E K R W R W R I N N S V F N G N V T N 154  
CGT GAA GAG AAA AGG TGG CGT TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC AAT 640

Q N Q N F N C A T I G L T K T F D A A S 174  
CAG AAT CAG AAT TTC AAC TGT GCG ACC ATT GGC CTA ACA AAG ACA TTT GAT GCT GCA TCA 700

C D I S Y R R I C E K N A K \* 188  
TGT GAC ATC AGC TAC CGC AGG ATC TGT GAG AAG AAT GCC AAA TGA 745

TCACAGTTCCCTGTGACAAAGAACTATACTTGCAACTCTTTTGAATCCATACAGGTCGTCTGGCCAATGATCTTTTAC 824  
TTACCTATCTGTCTACAGTAGCGGTCTTGCCCATTTGGGAAACTGAGCTTCTTTCTGCACTGGGGACTGGATG 903  
CTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCTGCTTCTGTAGTAC 982  
TGAGCATTTCTGACTGATCAAAAAGGCCCTAGTCTGTGACAGGTTTGTATTTTAGCCTCAGAGTATACCATATA 1061  
CTAGGAGTAACCTGTAGAGTGAGAAATATAAACAATATTAGGATFACCATGTGTGAAGAGGGATAAACAATAGGTCC 1140  
TGTGACTTCGTCTCTGTTCTCAAGGAAACCCCATTCACATGCCCTCCTAACTCCACAAGCAGGGTAGCAGAGGCTCT 1219  
CCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGAGCAGCATTTGTTT 1298  
ATGGGAATGGAGAGAGGTCTGGGACAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCCAGGAGCCAGGAGC 1377  
CAACACACTAGATTCTGTTCTTCAGCAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCTGAAGGTTTGTGAA 1456  
ACTCCATTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCTTGTCTCTGAAGGTTTGTGAGTA 1535  
CCTGGCTGTATTGTTGAGTATTTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCAATAATATTCATCCCTTC 1614  
AGTTCTGGAGAAAGCCTGATACAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATGTATCTA 1693  
GAACTGGTCCAGCCCGAAGAGTAGGAAAGAGAGGCTGCTCAGGAAACATTTGGCTGGGGGACCGGAATAAGCAC 1772  
ATAGTAAAAGGGAACATCAGGGTCAAAATGAAATCACTGAGACAGGAAACAGGGAGTTCAATTTGGCCACACTGGAAG 1851  
AAAGGCAAGAAAGAGGAAGACAAAGTCTTGGAGTACCTGGCTGTTCTCCACACTCAAGACATCAGCTATACTCTGCT 1930  
TGGTGCAATAAGAAAGAGATGCTTTTGTGTTTGTGAGTAAGAATAATTAACCAATAAGGAAGACCATGTATATA 2009  
AACTGATGGAAATAATAGTCAACCAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT 2088

Fig. 11B

ACATGTCATTGTATACCAACAAGATTGTTGTAAATCATATTTTTATTATTAACAACATAAGTTCTGCTTCTGCATT 2167  
 CCTAGGTTTCATCATTTTTTGGCTCCTTAGCATGGCCACTTACAAATTTTTTAACATGAGATAACACATCAGGTGTCAGAA 2246  
 CTTGCTTGAAGGAATTACCAGAAGTAATTTGTGTTTGAGATGGGTGGAATTTGGAATTATATTAGTAGCCGGTGGAG 2325  
 ATACAAGTTCTCTGACTGTGTTGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2404  
 AAATATCAACAGAACTCTAGCCAAGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGA 2483  
 GAAGAGAGAACTGTAGTTGCTTCACTTCCATTTCAATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACA 2562  
 TCTAGTGATTTCTTTAGTAGACAGTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAGGAGCCCA 2641  
 ATGGCCTGGGTGGGAGTAGATAGGGAATATGTGGGATTTTGGTTTAAAGTTTCATCATTTGGGAGAGTTCTCTGGA 2720  
 TCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGCGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTA 2799  
 GCAAGCCACTGAATTTGAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTCTTACCCTTCTCTGGT 2878  
 CTTAATTTCCTTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAAATTTATTGCACATATTAAATAACATTCCTCTA 2957  
 TGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT 3036  
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTCAGAACTTGTTTACTCATTTATAATATGGGAATA 3115  
 AAAAATTTGTGCAAGTCAGAGAAGGTGCCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATG 3194  
 ACCTCAAAATGTGGCCCAAGCTAGGTAGCCCAACCCCACTCCAACTTAGACTCACGAACAATCCACCTGAGATCAG 3273  
 CAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAAAATAAAAAAAA 3352  
 GTCTCTCGTATAGCAAAATCTAACTGATGCAATCTCCAATCTGGCCCTTCATCTCTCCCTTTATTGTCTCTTCGTGTAT 3431  
 TGTTCATCCAGCAACCAGGATGATCTTTGTTAAAAACATTAAACAGATTCTGTCAVKCTTTMAAAAAAAAAGGCCATGA 3510  
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACCTTTGGTTTCTAATAATGCTGTGTGAATCAGANCAGKTTTCTTACCCCT 3589  
 TTCTTGGTCTTAATTTCTGATAAAATGGGGTWGTAATACCTATCTCAAAAAATTTATGACATATTARATAACA 3668  
 TTCCCTCATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAG 3747  
 AAGTAGCTTTTCAATTTGSTAGAAAGCTTAATGTAGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATA 3826  
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAAGGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAGACACAC 3905  
 TTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTGAGCCCAACCCCACTCCAACTTAGACTCACGAACAAATCCACCT 3984  
 GAGATCAGCAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAATAAAAA 4063

AAAAAAAAAGAA 4074

Fig. 11C

GTGTCGCGCGGAGGTGAGACTGTGAAGAAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGC	79
CCCTGCTGCCACACCAAGCATTAGGCCACCAGGAAGACCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAG	158
M N W H M I I S G L I V V V	
GCCCCCTGCAGCTCCTTCATC ATG AAC TGG CAC ATG ATC TCT GGG CTT ATT GTG GTA GTG	14 220
L K V V G M T L F L L Y F P Q I F N K S	34
CTT AAA GTT GTT GGA ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT	280
N D G F T T T R S Y G T V S Q I F G S S	54
AAC GAT GGT TTC ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT	340
S P S P N G F I T T R S Y G T V S Q I F G S S	74
TCC CCA AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC	400
W E F Y Q A R C F F L S T S E S S W N E	94
TGG GAA TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA	460
S R D F C K G K G S T L A I V N T P E K	114
AGC AGG GAC TTT TGC AAA GGA AAA GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA	520
L K F L Q D I T D A E K Y F I G L I Y H	134
CTG AAG TTT CTT CAG GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT	580

Fig. 11D

R	E	E	K	R	W	R	W	I	N	N	S	V	F	N	G	K	Y	V	N	154
CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAG	TAC	GTG	AAC	640
M	P	Q	F	P	G	D	L	G	L	L	Q	K	T	K	P	E	I	A	G	174
ATG	CCA	CAG	TTT	CCT	GGG	GAT	CTT	GGT	TTG	CTT	CAA	AAG	ACC	AAA	CCT	GAG	ATT	GCT	GGG	700
F	T	L	E	*																178
TTC	ACC	CTG	GAA	TAG																715
CTCAA	ACGCTGACACT	GTGTTCTGCTCTTCTCCTTTCTTCCA	ACCATCTATTCCTATCTGTCTACCATAGC	794																
GGT	CCTTGCCCATTTGGG	AACTGAGCTTCTTCTTGCACTGGGGACTGGATGCTAGCCATCTCCAGGACAGGA	873																	
TCAGT	TTTACGGAAACAACTCAGT	TAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCAATTTCTGACTGATCAAAA	952																	
AGGC	TAGTCTGTGACAGGGTTGTTTATTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACTGTAGAGTGAG	1031																		
AAAT	TATAAACATTAATTAAGGATTAACCATGGTGAAGAGGATAAACATAGGTCCTGTGACTTCGTCTCTCTCAA	1110																		
GGAA	CCCCCATTCACATGCCCCCTCCTAACTCCACAAGCGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACCTAAGGCTTGG	1189																		
CCTT	GGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTATGGGAATGGAGAGGCTCTGGG	1268																		
CAGGA	TAGGAACCTTCTTGAGACCCCTTTGAAGAAAACCCAGGCAGCCAAAGGAGCCAAACACACTAGATTTCTGTTCT	1347																		
TCAGC	AAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCTATATTTCTGAAACTCCATTATAACATATGTAAC	1426																		
CCTTT	GTAAACCAAAATTTAGGTAAGCAGGCTTCCCTTTGCTCTGAAGGTTTGTAGTACCTGGCTGTATTTGTGAGTATT	1505																		
TTTAA	AAATTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTCATCCCTTCAGTTCTGGAGAAAGCCTGATACC	1584																		
AGGC	ACAGCCTACTGACCCCAAGGAGCCTGGCAGTGAATGGCATCACATTGATCTAGAACTGTGTCCAGCCGCCGAAGAG	1663																		
TAGG	AAAAGAGAAGGGCTGCTCAGGGAAACATTGGCTGGGGGCACGGAAATAAGCACATAGTAAAAAGGGAACATCAGGG	1742																		
TCAA	ATGGAATCACCTGAGACAGGAACACAGGGAGTTCAATTTGGCCACACTGGAAGAAAGGCAAGAAAGAGACAA	1821																		
GTCT	TGGAGTACCCCTGGCTGTTCTCCACACTCACAAAGACATCAGCTATACTCTGCTTGTGTCATAAGAAAGAGAAAAAGA	1900																		

Fig. 11E

GATGCCTTTTGTGTTTGAAGTAAGAAATTAACCATTAAGGAAGACCATGTATAAACTGATGGAAATAATAGTCACC 1979  
 AAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGTACATGTCATTGTATGTATACCAA 2058  
 ACAAGATTGTTGTAATCATATTTTATTACAAACACTAAGTTCTGCTTCTGCATTCTAGGTTTCATCATTTTGGCT 2137  
 CCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGAATTACCAGA 2216  
 AGTAATTTGTGTTGAGATGGGGTGGAAATTTGGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTG 2295  
 GGAAAGGATAAGTGCTACCGTTGAGAAAGGAAGAAAGGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2374  
 AAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTGGAGAAGAGAACTGTAGTTGCTTC 2453  
 ACTTCTATTTCATGACAGAAATACTGCAAAACCTTTAAGATCAGGAAATGTAGACATCTAGTGATTCTTTAGTAGACA 2532  
 GTTTAATTTCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAGGAGCCCCAATGGCCCTGGGTGGGAGTGGGA 2611  
 GTAGATAGGGAATATGTGGGATTGTTAAGTTTCATCATTTGGGAGAGTTCTCTGGATCCTTGCAAGCTTAGATAAATGT 2690  
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAATTTAGCAAGCCACTGAATTTGAGTTT 2769  
 CACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTCTTACCTTTTCTTGGTCTTAATTTCCTTACTGATAAAAT 2848  
 GGGTAGTAATACCTATCTCAAAAAATTATTGCACATATTAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2927  
 TAGGAGAAGCATTTTGTGGAGATTGAAAGTTGAGATCTTCATCCAAAGTAGCTTTTCAATTTGCTAGAAGCTTAAT 3006  
 GTAGGCAAGCCACTTCATTTTCAGAACTTGTACTCATTTATAATATGGGAATAAAATTTGTGCAAGTCAGAGAAG 3085  
 GGTGCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGCCCCAGCCTA 3164  
 GGTCAAGCAACCCCATCCAACTTATAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGATCAGCTGA 3243  
 AACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGTCTCTCGTATAGCAAAATCTAA 3322  
 CTGATGCAATCTCCATCTGGCTTCATCCTTCTCCCTTTATTGTCCCTTTCGTGATTGTTTCATCCAGCAACCAGGATGA 3401  
 TCTTGTAAAAACATTAAACAGATTCTGTCAKCTTMAAAAAAAGCCATGAAATNTAGCAAGCCACTGAATTT 3480  
 GAGTTTTCACCTTTGTTCTAATATGCTGTGAATCAGANCAKTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACT 3559  
 GATAAAATGGGTGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3638  
 TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGTAGCTTTTCAATTTGSTAGA 3717

Fig. 11F

AGCTTAATGTAGGCAAGCCACTTCAATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGT 3796  
 CAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTCATGACCTCAAATGTGGGC 3875  
 CCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGCAACAAATCCACCTGAGATCAGCAGAGCCACCTTAGA 3954  
 TCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAATAAAATAAAATAAA 4018

Fig. 11G

GAGACTGTGAAGAAGGAACGTTGCTTGGGCAAAAGGAGCATATTTCTCAGGAGACGGGGCCCTGCCTGCCACACCA 79  
 AGCATTAGGCCACAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGAGAAAGAGGCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V L K V V G 19  
 ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218

M T L F L L Y F P Q I F N K S N D G F T 39  
 ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC 278

T T R S Y G T V C P K D W E F Y Q A R C 59  
 ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 338

F F L S T S E S S W N E S R D F C K G K 79  
 TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA 398

G S T L A I V N T P E K L K F L Q D I T 99  
 GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT 458

Fig. 11H



D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	119
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	518
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	139
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	578
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	159
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	638
C	E	K	N	A	K	*														165
TGT	GAG	AAG	AAT	GCC	AAA	TGA														659
TCACAGTCCCTGTGACAAGAACTATACTTGCAACTCTTTTGAATCCATACAGGTCGTGGCCCAATGATCTTTTAC	738																			
TTACCTATCTGTCTACCAAGTAGCGGTCCTTGCCCATTTGGAAACTGAGCTTCTTCTGCACTGGGGACTGGATG	817																			
CTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTAC	896																			
TGAGCATTTCTGACTGATCAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTATTTTAGCCCTCAGAGTATACCATATA	975																			
CTAGGGAGTAACTGTAGAGTGAGAAATTATAAACATTATTTAGGGATTACCATGGTGAAGAGGGATAAACATAGGTCC	1054																			
TGTGACTTCGTCTGTCTCAAGGGAACCCCATTCACATGCCCTCCTAACTCCACAAGCGAGGTAGCAGAGGCTCT	1133																			
CCTCAGTCTGAACCTAAGGCTTGGCCTTGGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTT	1212																			
ATGGGAATGGAGAGGCTCTGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAAGGGAGC	1291																			
CAACACACTAGATTTCTGTTCTTCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCAATATTCTGAA	1370																			
ACTCCATTATAACATATGTAACCTCTTTGTAACCAAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTGTAGTA	1449																			
CCTGGCTGTATTTGTTGAGTATTTTAAAAATTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATCATCCCTTC	1528																			
AGTTCTGGAGAAAAGCCTGATACCAAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATGGCATCACATTGATCTA	1607																			

Fig. 11I

GAACTGGTCCAGCCGCGAAGAGTAGGAAAAGAGAAGGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAATAAGCAC 1686  
 ATAGTAAAAAGGGAACATCAGGGTCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAAG 1765  
 AAAGCAAGAAAGAGGAAAGACAGTCTTGGAGTACCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCT 1844  
 TGGTGCAATAAGAAAGAGAAAGAGATGCCTTTTGTGTTTGTAGTAAGAATAATAAACCATATAAGGAAGACCATGTATAA 1923  
 AACTGATGGAAATAATAGTCACCAAAAGTACAGCACATACCATTTTGTGCTCTAATAACAATGTAGCACAGTAATGACTGT 2002  
 ACATGTCATTGTATGTATACCAAAACAAGATTGTTGTAATCATATTTTATTATTAACAACATAAGTTCTGCTTCTGCATT 2081  
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAA 2160  
 CTTGCTTGAAGGGAATTACAGAAAGTAATTTGTGTTTGTAGATGGGTGGAAATTGGAATTATATTAGTAGCCGGTGGAG 2239  
 ATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2318  
 AAATATCAACAGAACTCTAGCCAAAGCAAGCCCGAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTGA 2397  
 GAAGAGAACTGTAGTTGCTTCACTTCCATTTTATGACAGAATAACTGCAAACTTTTAAAGATCAGGAAATGTAGACA 2476  
 TCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCA 2555  
 ATGGCCCTGGGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAGTTTCATCATTTGGGAGAGTTCCTGGA 2634  
 TCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGCAATGAAAATTTA 2713  
 GCAAGCCACTGAATTTGAGTTTTCACTTTGTCTTAATATGCTGTGTAATCAGTACAGTTTCTTACCCTTTCTTGGT 2792  
 CTTAATTTCTTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAAATTATTGCACATATTAAATAACATTCCTCTA 2871  
 TGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT 2950  
 TTTCAAATTTGCTAGAAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTCTACTCATTTATAATATGGGAATA 3029  
 AAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAGACACACTTTTCATG 3108  
 ACCTCAAATGTGGCCAGCCTAGGTAGCCAAACCCCATCCAACTTAGACTCAGCAACAAATCCACCTGAGATCAG 3187  
 CAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCAGTGTAAAAAAAATAAAAAAAA 3266  
 GTCTCTCGTATAGCAAAAATCTAACTGATGCAATCTCCATCTGGCCCTTCATCCTTCTCCCTTTATTGTCCCTTTCGTAT 3345  
 TGTTCATCCAGCAACCAGGATGATCTTGTAAAAACATTAAACAGATTCTGTCAKCTTTMAAAAAAAAAGCCATGA 3424  
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACCTTGGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCT 3503

Fig. 11J

TTCTTGGTCTTAATTTCCTTACTGATAAAAATGGGTGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACA 3582  
 TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAGCATTTTGTGGAGGATTGGAAGTTGAGATCTTTCATCCCAAG 3661  
 AAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTATAATA 3740  
 TGGGAATAAAAAATTGTGCAAGTCAGAGAAGGTGCCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAAGACACAC 3819  
 TTTTCATGACCTCAAAATGTGGGCCAGCCCTAGGTCAGCCCAACCCCATCCAAACCTTAGACTCAGGAACAAATCCACCT 3898  
 GAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 3977  
 AAAAAAA 3985

Fig. 11K

GAGACTGTGAAGAAGGAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCA 79  
 AGCATTAGGCCACCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGAGAAAGAGGCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V V L K V V G 19  
 ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218  
 M T L F L L Y F P Q I F N K S N D G F T 39  
 ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC 278  
 T T R S Y G T V C P K D W E F Y Q A R C 59  
 ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 338

Fig. 11L

F	F	L	S	T	S	E	S	S	W	N	E	S	R	D	F	C	K	G	K				79
TTT	TTC	TTA	TCC	ACT	TCT	GAA	TCA	TCT	TGG	AAT	GAA	AGC	AGG	GAC	TTT	TGC	AAA	GGA	AAA			398	
G	S	T	L	A	I	V	N	T	P	E	K	L	K	F	L	Q	D	I	T			99	
GGA	TCC	ACA	TTG	GCA	ATT	GTC	AAC	ACG	CCA	GAG	AAA	CTG	AAG	TTT	CTT	CAG	GAC	ATA	ACT			458	
D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W			119	
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG			518	
I	N	N	S	V	F	N	G	K	Y	V	N	M	P	Q	F	P	G	D	L			139	
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAG	TAC	GTG	AAC	ATG	CCA	CAG	TTT	CCT	GGG	GAT	CTT			578	
G	L	L	Q	K	T	K	P	E	I	A	G	F	T	L	E	*						155	
GGT	TTG	CTT	CAA	AAG	ACC	AAA	CCT	GAG	ATT	GCT	GGG	TTC	ACC	CTG	GAA	TAG						629	
CTCAA	ACGCTGACACTTGACTCTGTTCTGCTCTTCTCCTTTCTTCCAA	ACCCATCTATTCCCTATCTGTCTACCATAGC																				708	
GGTCCTTGCCCATTTGGGAAACTGAGCTTCTTTCTGCACTGGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA																						787	
TCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCAATTTCTGACTGATCAAAA																						866	
AGGCCTAGTCTGTTGACAGGGTTTGTATTTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACTGTAGAGTGAG																						945	
AAATTATAAACATTATTTAGGATTACCATGGTGAAGAGGGATAAACATAGGTCCCTGTGACTTCGTCTCTGTCTCAA																						1024	
GGGAACCCCATTCACATGCCCTCCTAACTCCACAAGCGAGGGTAGCAGGGCTCTCCTCAGTCTGAACCTAAGGCTTGG																						1103	
CCTTGGGGAGGGCTCCTAGTGCTGAGCTTGGAGCAGCACGGACAGCATTTGTTATGGGAATGGAGAGAGGTCTGGG																						1182	
CAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAAACAGGCAGCCAAAGGGAGCCAAACACACTAGATTTCTGTTCT																						1261	
TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAAATCCCTTGTCAATTTCTGAAACTCCATTATAACATATGTAAC																						1340	

Fig. 11M

CCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCCTTTGCTCTGAAGGTTTTTGAGTACCTGGCTGTATTTGTTGAGTATT 1419  
 TTTAAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATTCATCCCTTCAGTTCTGGAGAAAAGCCCTGATACC 1498  
 AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTCAGAACTGATCTAGAACTGGTCCAGCCGCCGAAGAG 1577  
 TAGGAAAAGAGAAGGCTGCTCAGGGAACATTTGGCTGGGACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1656  
 TCAAAATGGAAATCACCTGAGACAGGAACACAGGGAGTTTCATTTGGCCACACTGGAGAAAGGCAAGAAAGAGGAACAA 1735  
 GTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAAGACATCAGCTATATCTCTGCTTGGTGATAGAAAAGAGAAAAGA 1814  
 GATGCCCTTTTGTGTTTGAAGTAAGAATAATAAACCATAGGAAGACCATGTATAAACTGATGGAATAATAGTCACC 1893  
 AAAGTACAGCACATACCAATTTTGTGCTAAATAACAATGTAGCACAGTAATGACTGTACATGTTCATTTGTATGTATACCAA 1972  
 ACAAGATTGTTGTAAATCATATTTTTTTATTACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTTGGCT 2051  
 CCTTAGCATGCCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAGGGAATTACCAGA 2130  
 AGTAATTTGTGTTTGAATGGGTGGAATTTGAATTTATATTAGTAGCCGGTGAGATACAAAGTTCTCTGACTGTGTTG 2209  
 GGAAAGGATAAGTGCTACCGTTGAGAAAGGGAAGAGGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2288  
 AAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAGAGAGAACTGTAGTTGCTTC 2367  
 ACTTCCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2446  
 GTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAAGTTCTAAAGAGGCCCAATGGCCTGGGTGGGAGTGGGA 2525  
 GTAGATAGGGAATATGTGGGATTTGGTTTAAGTTTCATCATTTGGGAGAGTTCCCTGGATCCTTGCAAGCTTAGATAAATGT 2604  
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGCAATGAAATTTAGCAAGCCACTGAATTTGAGTTT 2683  
 CACTTTGTTTCTAAATATGCTGTGAATCAGTACAGTTTCTTACCCTTTCTTGGTCTTAAATTTCTTACTGATAAAAT 2762  
 GGGTAGTAATACCTATCTCAAAAAATTTATGCACATATTTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2841  
 TAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAGAAGTAGCTTTTCAATTTGCTAGAAAGCTTAAT 2920  
 GTAGGCAAGCCACTTCATTTTTCAGAACTTTTACTCATTTATAATATGGAAATAAAATTTGTGCAAGTCAGAGAAG 2999  
 GGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACACTTTTTCATGACCTCAAAATGTGGGCCCCAGCCTA 3078  
 GGTGAGCCCAACCCCATCCACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCTAGATCAGCTGA 3157  
 AACTCTAAGCACAAAAATAAAAACCTTATCACTGTAAAAAAAAGTCTCTCGTATAGCAAAATCTAA 3236

Fig. 11N

CTGATGCAATCTCCATCTGGCCCTTCATCCCTTTATTTGTCCTTTTCGTGTATTGTTTCATCCAGCAACCAGGATGA 3315  
TCTTGTTAAAAACATTAAACAGATTCTGTCAKCTTTMAAAAAAAGCCATGAAATTTNTAGCAAGCCACTGAATTT 3394  
GAGTTTTCACCTTTGGTTCTAATATGCTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCTTAATTTCCCTTACT 3473  
GATAAAATGGGTGTAATACCTATCTCAAAAAATTTATGACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3552  
TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAAGTTGAGATCTTCATCCAGAGTAGCTTTTCAATTTTGSTAGA 3631  
AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTATAATATGGGAATAAAAAATTTGTGCAAGT 3710  
CAGAGAAGGTGCCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGC 3789  
CCAGCCTAGGTCAGCCAAACCCCATCCAACTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGA 3868  
TCAGCTGAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAACGACCTGCCCG 3947  
GGCGGCCGCC 3958

Fig. 110

GAGACTGTGAAGAAGGAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCTGCCTGCCACACCA 79  
AGCATTAGGCCACCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V L K V V G 19  
ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218  
M T L F L L Y F C P K D W E F Y Q A R C 39  
ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 278  
F F L S T S E S S W N E S R D F C K G K 59  
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA 338

Fig. 11P

G	S	T	L	A	I	V	N	T	P	E	K	L	K	F	L	Q	D	I	T	79
GGA	TCC	ACA	TTG	GCA	ATT	GTC	AAC	ACG	CCA	GAG	AAA	CTG	AAG	TTT	CTT	CAG	GAC	ATA	ACT	398
D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	99
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	458
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	119
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	518
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	139
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	578
C	E	K	N	A	K	*														145
TGT	GAG	AAG	AAT	GCC	AAA	TGA														599
TCACAGTCCCTGTGACAAGAACTATACTTGCAACTCTTTTGAATCCATACAGGTCGTGGCCAATGATTCCTTTAC	678																			
TTACCTATCTGTCTACAGTAGCGGTCCTTGCCCATTTGGGAAACTGAGCTTCTTTCTGCACTGGGGACTGGATG	757																			
CTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTAC	836																			
TGAGCATTTCTGACTGATCAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTATTTTAGCCCTCAGAGTATACCATACTA	915																			
CTAGGGAGTAAGTGTAGAGTGAGAAATTATAAACATTATTAGGATTACCATGTTGGAAGAGGATAAACATAGGTCC	994																			
TGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCTCCTAACTCCACAAAGCGAGGTAGCAGAGGCTCT	1073																			
CCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTGTGAGCTTGAGCAGCACGGACAGCAGCATTTGTTT	1152																			
ATGGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAGGGAGC	1231																			

Fig. 11Q

CAAACACACTAGATTTCTGTTCTTTCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCAATATTTCTGAA 1310  
 ACTCCATTATAACATATGTAACCTCTTTGTAAACCAAAATTTAGGTAAAGCAGGCTTCCTTTGTCTCTGAAGGTTTTTGAGTA 1389  
 CCTGGCTGTATTTGTTGAGTATTTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTCATCCCTTC 1468  
 AGTCTGGAGAAAGCCTGATACAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA 1547  
 GAACTGGTCCAGCCCGGAAGAGTAGGAAAAGAGAAGGGCTGCTCAGGGAAACATTTGGCTGGGGGCACGGAATAAGCAC 1626  
 ATAGTAAAAAGGGAACATCAGGGTCAATGGAATCACCTGAGACAGGAAACAGGGAGTTCAATTTGGCCACACTGGAAG 1705  
 AAAGGCAAGAAAGAGGAAGACAAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAAGACATCAGCTATACTCTGCT 1784  
 TGGTGCAATAAGAAAGAGAAAGAGATGCCCTTTTGTGTTTGAGTAAAGAAATAATTAAACCATAAAGGAAGACCATGTATAA 1863  
 AACTGATGGAAATAATAGTCACCAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT 1942  
 ACATGTCATTGTATGTATACCAACAAGATTGTTGTAATCATATTTTATTACAACACTAAGTTCTGCTTCTGCATT 2021  
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAA 2100  
 CTTGCTTGAAAGGAATTACCAGAAAGTAATTTGTGTTTGAGATGGGTGGAAATTGGAATTATATTAGTAGCCGGTGGAG 2179  
 ATACAAAGTTCTCTGACTGTGTTGGAAAGGATAAGTGTACCGTTGAGAAAGGAGAAAGGCTGAGTCTAGGTGGAGAA 2258  
 AAATATCAACAGAACTCTAGCCAAAGCAAGCCCAAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGA 2337  
 GAAGAGAGAACTGTAGTTGCTTCACCTTCCCTATTTCATGACAGAATAACTGCAAAACCTTTAAAGATCAGGAAATGTAGACA 2416  
 TCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCA 2495  
 ATGGCCCTGGGTGGGAGTAGAGGGAATATGTGGGATTTGGTTAAAGTTTCATCATTTGGGAGAGTTCCTGGA 2574  
 TCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTA 2653  
 GCAAGCCACTGAATTTGAGTTTTCACCTTTGTTTCTAATAATGCTGTGTAATCAGTACAGTTTTCCTACCCCTTCTTGGT 2732  
 CTTAATTTCCCTACTGATAAAATGGGTAGTAATACCTATCTCAAAAAATATTGCACATATTAATAAACATTCCCTCTA 2811  
 TGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAGTAGCT 2890  
 TTTCAATTTGCTAGAAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAAATATGGGAATA 2969  
 AAAATTTGTGCAAGTCAGAGAAAGGTGCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACTTTTCATG 3048  
 ACCTCAATGTGGGCCAGCCTAGGTACGCCAACCCCATCCACCTTAGACTCACGAACAATCCACCTGAGATCAG 3127

Fig. 11R



CAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCAGCTGTAAAAAATAAAAAAATAAAAAA 3206  
 GTCCTCTGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCCTTTCGTGTAT 3285  
 TGTTCAATCCAGCAACCAGGATGATCTTGTAAACATTAACAGATTCTGTCAYKCTTTMAAAAAAATAAGCCATGA 3364  
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACCTTTGTTCTAATAATGCTGTGTGAATCAGANCAGKTTTCTTACCT 3443  
 TTCTTGGTCTTAATTTCCCTTACTGATAAAATGGGGTGTAAATACCTATCTCAAAAAATTATTGCACATATTARATAACA 3522  
 TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTGAAGTTGAGATCTTCATCCAAG 3601  
 AAGTAGCTTTTCAATTTGSTAGAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATA 3680  
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAGACACAC 3759  
 TTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCACCTTAGACTCACGAACAAATCCACCT 3838  
 GAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 3917  
 AAAAAAA 3925

Fig. 11S

GAGACTGTGAAGAAAGAACGTTGCTTGGGCAAAAGAGAGCATATTCTCAGGAGACGGGGCCCCCTGCCACACCA	79
AGCATTAGGCCACCCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC	158
M      N      W      H      M      I      I      S      G      L      I      V      V      L      K      V      V      G	19
ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	218
M      T      L      F      L      L      Y      F      C      P      K      D      W      E      F      Y      Q      A      R      C	39
ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	278
F      F      L      S      T      S      E      S      S      W      N      E      S      R      D      F      C      K      G      K	59
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA	338
G      S      T      L      A      I      V      N      T      P      E      K      L      K      F      L      Q      D      I      T	79
GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT	398
D      A      E      K      Y      F      I      G      L      I      Y      H      R      E      E      K      R      W      R      W	99
GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT CGT GAA GAG AAA AGG TGG CGT TGG	458
I      N      N      S      V      F      N      G      K      Y      V      N      M      P      Q      F      P      G      D      L	119
ATC AAC AAC TCT GTG TTC AAT GGC AAG TAC GTG AAC ATG CCA CAG TTT CCT GGG GAT CTT	518
G      L      L      Q      K      T      K      P      E      I      A      G      F      T      L      E      *	135
GGT TTG CTT CAA AAG ACC AAA CCT GAG ATT GCT GGG TTC ACC CTG GAA TAG	569

Fig. 11T

CTCAAACGCTGACACTTGACTCTGTTCTGCTCTTCTCCTTTCTTCCAACCCATCTATTCCCCTATCTGTCTACCAGTAGC 648  
GGTCCTTGCCCATTTGGGAAACTGAGCTTCTTCTTGCACTGGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA 727  
TCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGATCAAAA 806  
AGGCCTAGTCTGTTGACAGGGTTTGTATTTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACCTGTAGAGTGAG 885  
AAATTATAAACATTATTTAGGGATTACCATGGTGGAAAGGGATAAACATAGTCCCTGTGACTTCGTCTCTCTCAA 964  
GGAAACCCCATTCACATGCCCCCTCCTAACTCCACAAGCGAGGTAGCAGAGGCTCTCCTCAGTCTGAACCTAAGGCTTGG 1043  
CCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGGACAGCATTTGTTATGGGAATGGAGAGAGGTCTGGG 1122  
CAGGATAGGAACCTTCTTGGAGACCCCCTTTGAAAGAAAACCAGGCAGCCAGGGAGCCAAACACACTAGATTTCTGTTCT 1201  
TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCTATATTTCTGAACTCCATTATAACATATGTAACT 1280  
CCTTTGTAACCAAATTTAGGTAAGCAGGCTTCTTGTCTGAAGGTTTGTAGTACCTGGCTGTATTTGTTGAGTATT 1359  
TTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTCACTCCCTTCAGTTCTGGAGAAAAGCCTGATACC 1438  
AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTAGAACTGGTCCAGCCGCCGAAGAG 1517  
TAGGAAAAGAGAAGGGCTGCTCAGGAAACATTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1596  
TCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAAAGAAAGGCAAGAGGAAGACAA 1675  
GTCTTGGAGTACCCCTGGCTGTTCTCCACACTCAACAAGACATCAGCTATACTCTGCTTGGTGCATAGAAAGAGAAAAGA 1754  
GATGCCCTTTGTGTTTGTAGTAAGAATAATTAACCATTAAGGAAGACCATGTATAAACTGATGGAATAAATAGTCACC 1833  
AAAGTACAGCACATACCAATTTGTGCTAATAACAATGTAGCACAGTAATGACTGTACATGTTCATTTGTATATACCAA 1912  
ACAAGATTGTTGTAAATCATATTTTATTATACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCT 1991  
CCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAAGAACTTGCTTGAAGGGAATTACCAGA 2070  
AGTAATTTGTGTTTGTAGATGGGTGGAATTTGGAATTTATATTAGTACCGGTGGAGATACAAGTTCTCTGACTGTGTG 2149  
GGAAGGATAAGTGCTACCGTTGAGAAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAAAATAATCAACAGAACTCTAGCCA 2228  
AAGGCAAGCCCCAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGTAGAAAGAGAACTGTAGTGTCTC 2307  
ACTTCCCTATTTCATGACAGAATAACTGCAAACCTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2386

Fig. 11U

GTTTAAATTTCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAGAGGCCCAATGGCCTGGGTGGAGTGGGA 2465  
 GTAGATAGGGAATATGTGGGATTGGTTTAAAGTTTCATCATTTGGGAGAGTTCTCTGGATCCTTGCAAGCTTAGATAAAATGT 2544  
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGCAATGAAATTTAGCAAGCCACTGAAATTTGAGTTT 2623  
 CACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTCTTACCCTTTCTTGGTCTTAATTTCTTACTGATAAAAT 2702  
 GGGTAGTAATACCTATCTCAAAAAATTTATTGCACATATTAAATAACATTCCCTCTATGTATCTCAATGGCATTAGACAT 2781  
 TAGGAGAAGCAATTTGTGGAGGATTTGAAGTTGAGATCTTTCATCCAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAAT 2860  
 GTAGGCAAGCCACTTCATTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 2939  
 GGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAGACACACTTTTCATGACCTCAAAATGTGGCCAGCCTA 3018  
 GGTCAAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGATCAGCTGA 3097  
 AACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAGAAAAAGTCTCTCGTATAGCAAAATCTAA 3176  
 CTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTATTGTCCTTTCGTGTATTGTTTCATCCAGCAACCAGGATGA 3255  
 TCTTGTTAAAAACATTAAACAGATTCTGTCAKCTTTMAAAAAAAGCCATGAAATNTAGCAAGCCACTGAATTT 3334  
 GAGTTTTCACCTTTGGTTTCTAATATGCTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCTTAAATTTCCCTTACT 3413  
 GATAAAATGGGTGTAATACCTATCTCAAAAAATATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3492  
 TTAGACATTAGGAGAAGCAATTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAGAAAGTAGCTTTTCAATTTGSTAGA 3571  
 AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGT 3650  
 CAGAGAAGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAGACACACACTTTTCATGACCTCAAATGTGGGC 3729  
 CCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGA 3808  
 TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAGAAAAAAGAAAGAACCTTGCCCCG 3887  
 GGCGGCGCGCCC 3898

Fig. 11V

10		20		30		40		50		60		70		80		90		100	
M	MNWHMIISGLIVVVIKVVGMTFFLLYFPQVFGKNSDGFVPTESYGTTSVQNVSQIFGRNDESTMPTRSYGTVCPRNWDHFHQKCFFFSFSESPWKDSMDY																		
R	MNWHMIISGLIVVVIKVVGMTFFLLYFPQVFGKNSDGFVPTESYGTTSVQNVSQIFGRNDESTMPTRSYGTVCPRNWDHFHQKCFFFSFSESPWKDSMDY																		
H	MNWHMIISGLIVVVLKVVGMTLFLLYFPQIFNKNSDGFTTTTSYGT--VSQIFGSSSPSPNGFITTTTSYGTVCPCPDWEFYQARCFLLSTSESSWNE SRDF																		
A	MNWHMIISGLIVVVLKVVGMTLFLLYFPQIFNKNSDGFTTTTSYGT--VSQIFGSSSPSPNGFITTTTSYGTVCPCPDWEFYQARCFLLSTSESSWNE SRDF																		
C	MNWHMIISGLIVVVLKVVGMTLFLLYFPQIFNKNSDGFTTTTSYGT--V-----CPKDWEFYQARCFLLSTSESSWNE SRDF																		
E	MNWHMIISGLIVVVLKVVGMTLFLLYF-----CPKDWEFYQARCFLLSTSESSWNE SRDF																		
B	MNWHMIISGLIVVVLKVVGMTLFLLYFPQIFNKNSDGFTTTTSYGT--VSQIFGSSSPSPNGFITTTTSYGTVCPCPDWEFYQARCFLLSTSESSWNE SRDF																		
D	MNWHMIISGLIVVVLKVVGMTLFLLYFPQIFNKNSDGFTTTTSYGT--V-----CPKDWEFYQARCFLLSTSESSWNE SRDF																		
F	MNWHMIISGLIVVVLKVVGMTLFLLYF-----CPKDWEFYQARCFLLSTSESSWNE SRDF																		

110		120		130		140		150		160		170		180	
M	CATQGSTLAIVNTPEKLKYLQDIAGIENYFIGLVRQPGEKKRWINNSVFNGNVTNQDQNFDCVTIGLTKTYDAASCEVS YRWICEMNAK														
R	CATQGSTLAIVNTPEKLKYLQDIAGIENYFIGLVRQPGEKKRWINNSVFNGNVTNQDQNFDCVTIGLTKTYDAASCEVS YRWICEMNAK														
H	CKGKGSTLAIVNTPEKL-FLQDITDAEKYFIGLIYHREEKRWINNSVFNGNVTNQDQNFDCVTIGLTKTYDAASCDIS YRRICEKNAK														
A	CKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWINNSVFNGNVTNQDQNFDCVTIGLTKTYDAASCDIS YRRICEKNAK														
C	CKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWINNSVFNGNVTNQDQNFDCVTIGLTKTYDAASCDIS YRRICEKNAK														
E	CKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWINNSVFNGNVTNQDQNFDCVTIGLTKTYDAASCDIS YRRICEKNAK														
B	CKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWINNSVFNGKYVNMPPQDGLGLLQTKTKPEIAGFTLE														
D	CKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWINNSVFNGKYVNMPPQDGLGLLQTKTKPEIAGFTLE														
F	CKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWINNSVFNGKYVNMPPQDGLGLLQTKTKPEIAGFTLE														

Fig. 11W

# Figure 11X-1

	10	20	30	40	50	60	70	80	90	100
A	GTGGTCGGCCGAGGTGAGACTGTGAAGAAGGAAGAACGTTGCTTGGGCAAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
B	GTGGTCGGCCGAGGTGAGACTGTGAAGAAGGAAGAACGTTGCTTGGGCAAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
C	GAGACTGTGAAGAAGGAAG-----AACGTTGCTTGGGCAAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
D	GAGACTGTGAAGAAGGAAG-----AACGTTGCTTGGGCAAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
E	GAGACTGTGAAGAAGGAAG-----AACGTTGCTTGGGCAAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
F	GAGACTGTGAAGAAGGAAG-----AACGTTGCTTGGGCAAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
	110	120	130	140	150	160	170	180	190	200
A	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAAGAGGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
B	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAAGAGGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
C	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAAGAGGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
D	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAAGAGGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
E	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAAGAGGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
F	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAAGAGGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
	210	220	230	240	250	260	270	280	290	300
A	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATGACCTTATTCTACTTTATTTCCCAACAGATTTTAAACAAAAGTAACGATGGTTTCACCAACCAC									
B	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATGACCTTATTCTACTTTATTTCCCAACAGATTTTAAACAAAAGTAACGATGGTTTCACCAACCAC									
C	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATGACCTTATTCTACTTTATTTCCCAACAGATTTTAAACAAAAGTAACGATGGTTTCACCAACCAC									
D	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATGACCTTATTCTACTTTATTTCCCAACAGATTTTAAACAAAAGTAACGATGGTTTCACCAACCAC									
E	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATGACCTTATTCTACTTTATT-----									
F	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATGACCTTATTCTACTTTATT-----									

Fig. 11X-1

	310	320	330	340	350	360	370	380	390	400
A	CAGGAGCTATGGAACAGTCTCACAGATTTTGGGAGCAGTTCCCAAGTCCCAACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCAAAGAC									
B	CAGGAGCTATGGAACAGTCTCACAGATTTTGGGAGCAGTTCCCAAGTCCCAACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCAAAGAC									
C	CAGGAGCTATGGAACAG-----TCTGCCCCAAAGAC									
D	CAGGAGCTATGGAACAG-----TCTGCCCCAAAGAC									
E	-----TCTGCCCCAAAGAC									
F	-----TCTGCCCCAAAGAC									
	410	420	430	440	450	460	470	480	490	500
A	TGGGAATTTTATCAAGCAAGATGTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA									
B	TGGGAATTTTATCAAGCAAGATGTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA									
C	TGGGAATTTTATCAAGCAAGATGTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA									
D	TGGGAATTTTATCAAGCAAGATGTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA									
E	TGGGAATTTTATCAAGCAAGATGTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA									
F	TGGGAATTTTATCAAGCAAGATGTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA									
	510	520	530	540	550	560	570	580	590	600
A	TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAAAGTCTGAGAAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
B	TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAAAGTCTGAGAAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
C	TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAAAGTCTGAGAAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
D	TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAAAGTCTGAGAAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
E	TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAAAGTCTGAGAAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
F	TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAAAGTCTGAGAAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									

Fig. 11X-2

Figure 11X-3

	610	620	630	640	650	660	670	680	690	700
A	TTGGATCAACAAC	CTGTGTTCAAT	GGCAATGTTAC	CAATCAGAAT	CAGAATTTCA	ACTGTGCGAC	CAATGGCC	TAAACAAAG	ACATTTGAT	GCTGCATCA
B	TTGGATCAACAAC	CTGTGTTCAAT	GGCAAGTACG	TGAACATGCC	ACAGTTCC	TGGGATCTTG	GTTCCTTCA	AAAGACCA	ACCTGAGAT	TGCTGGG
C	TTGGATCAACAAC	CTGTGTTCAAT	GGCAATGTTAC	CAATCAGAAT	CAGAATTTCA	ACTGTGCGAC	CAATGGCC	TAAACAAAG	ACATTTGAT	GCTGCATCA
D	TTGGATCAACAAC	CTGTGTTCAAT	GGCAAGTACG	TGAACATGCC	ACAGTTCC	TGGGATCTTG	GTTCCTTCA	AAAGACCA	ACCTGAGAT	TGCTGGG
E	TTGGATCAACAAC	CTGTGTTCAAT	GGCAATGTTAC	CAATCAGAAT	CAGAATTTCA	ACTGTGCGAC	CAATGGCC	TAAACAAAG	ACATTTGAT	GCTGCATCA
F	TTGGATCAACAAC	CTGTGTTCAAT	GGCAAGTACG	TGAACATGCC	ACAGTTCC	TGGGATCTTG	GTTCCTTCA	AAAGACCA	ACCTGAGAT	TGCTGGG
	710	720	730	740	750	760	770	780	790	800
A	TGTGACATCAG	CTACCGCAGG	ATCTGTGAGA	AGAAATGCC	AAATGATCAC	AGTTCCTGTG	ACAGAACTA	TACTTGCA	ACTCTTTT	TGAATCCATACAGG
B	TTCACCC	TGGAATAG	CTCAAACG	CTGACACT	TGACTCTGT	CTCTCTT	CTTCTCA	ACCCATCT	ATTC-----	
C	TGTGACATCAG	CTACCGCAGG	ATCTGTGAGA	AGAAATGCC	AAATGATCAC	AGTTCCTGTG	ACAGAACTA	TACTTGCA	ACTCTTTT	TGAATCCATACAGG
D	TTCACCC	TGGAATAG	CTCAAACG	CTGACACT	TGACTCTGT	CTCTCTT	CTTCTCA	ACCCATCT	ATTC-----	
E	TGTGACATCAG	CTACCGCAGG	ATCTGTGAGA	AGAAATGCC	AAATGATCAC	AGTTCCTGTG	ACAGAACTA	TACTTGCA	ACTCTTTT	TGAATCCATACAGG
F	TTCACCC	TGGAATAG	CTCAAACG	CTGACACT	TGACTCTGT	CTCTCTT	CTTCTCA	ACCCATCT	ATTC-----	
	810	820	830	840	850	860	870	880	890	900
A	TCGCTGGCCAA	TGATCTTTT	TACTTACCTA	TCTGTCTACC	AGTAGCGG	TCCCTTGCC	CAATTTGG	AAACTGAG	CTCTTTCT	TCTGCAC
B	-----									
C	TCGCTGGCCAA	TGATCTTTT	TACTTACCTA	TCTGTCTACC	AGTAGCGG	TCCCTTGCC	CAATTTGG	AAACTGAG	CTCTTTCT	TCTGCAC
D	-----									
E	TCGCTGGCCAA	TGATCTTTT	TACTTACCTA	TCTGTCTACC	AGTAGCGG	TCCCTTGCC	CAATTTGG	AAACTGAG	CTCTTTCT	TCTGCAC
F	-----									

Fig. 11X-3



Figure 11X-4

910		920		930		940		950		960		970		980		990		1000
A	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT																	
B	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT																	
C	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT																	
D	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT																	
E	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT																	
F	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGAT																	
1010		1020		1030		1040		1050		1060		1070		1080		1090		1100
A	CAAAAAGGCCTAGTCTGTGACAGGGTTTGTATTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACCTGTAGAGTGAGAAATTATAAACATTAT																	
B	CAAAAAGGCCTAGTCTGTGACAGGGTTTGTATTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACCTGTAGAGTGAGAAATTATAAACATTAT																	
C	CAAAAAGGCCTAGTCTGTGACAGGGTTTGTATTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACCTGTAGAGTGAGAAATTATAAACATTAT																	
D	CAAAAAGGCCTAGTCTGTGACAGGGTTTGTATTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACCTGTAGAGTGAGAAATTATAAACATTAT																	
E	CAAAAAGGCCTAGTCTGTGACAGGGTTTGTATTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACCTGTAGAGTGAGAAATTATAAACATTAT																	
F	CAAAAAGGCCTAGTCTGTGACAGGGTTTGTATTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACCTGTAGAGTGAGAAATTATAAACATTAT																	
1110		1120		1130		1140		1150		1160		1170		1180		1190		1200
A	TTAGGGATTACCATGGTGGAAAGAGGGGATAAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG																	
B	TTAGGGATTACCATGGTGGAAAGAGGGGATAAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG																	
C	TTAGGGATTACCATGGTGGAAAGAGGGGATAAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG																	
D	TTAGGGATTACCATGGTGGAAAGAGGGGATAAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG																	
E	TTAGGGATTACCATGGTGGAAAGAGGGGATAAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG																	
F	TTAGGGATTACCATGGTGGAAAGAGGGGATAAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAG																	

**Fig. 11X-4**

Sequence

	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
A	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTAT									
B	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTAT									
C	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTAT									
D	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTAT									
E	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTAT									
F	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTAT									
	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
A	GGGAATGGAGAGAGGCTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCCAAAGGAGGCCAAACACACTAGATTCTGTCTCT									
B	GGGAATGGAGAGAGGCTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCCAAAGGAGGCCAAACACACTAGATTCTGTCTCT									
C	GGGAATGGAGAGAGGCTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCCAAAGGAGGCCAAACACACTAGATTCTGTCTCT									
D	GGGAATGGAGAGAGGCTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCCAAAGGAGGCCAAACACACTAGATTCTGTCTCT									
E	GGGAATGGAGAGAGGCTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCCAAAGGAGGCCAAACACACTAGATTCTGTCTCT									
F	GGGAATGGAGAGAGGCTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCCAAAGGAGGCCAAACACACTAGATTCTGTCTCT									
	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
A	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTTCATATTCTGAAACTCCATTTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGG									
B	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTTCATATTCTGAAACTCCATTTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGG									
C	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTTCATATTCTGAAACTCCATTTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGG									
D	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTTCATATTCTGAAACTCCATTTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGG									
E	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTTCATATTCTGAAACTCCATTTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGG									
F	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTTCATATTCTGAAACTCCATTTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGG									

Fig. 11X-5

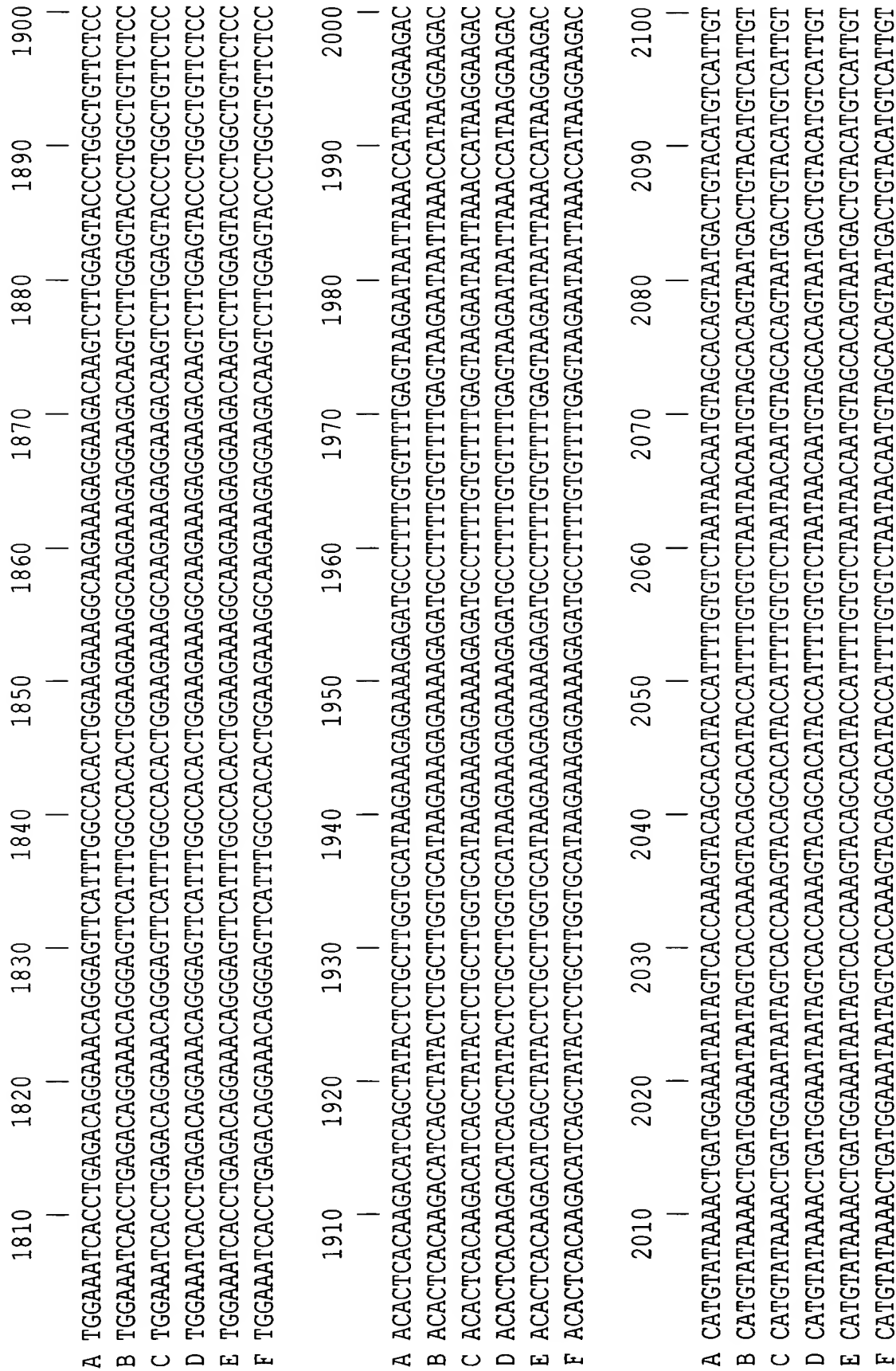


Fig. 11X-7

# FIG. 10 "DETAILED"

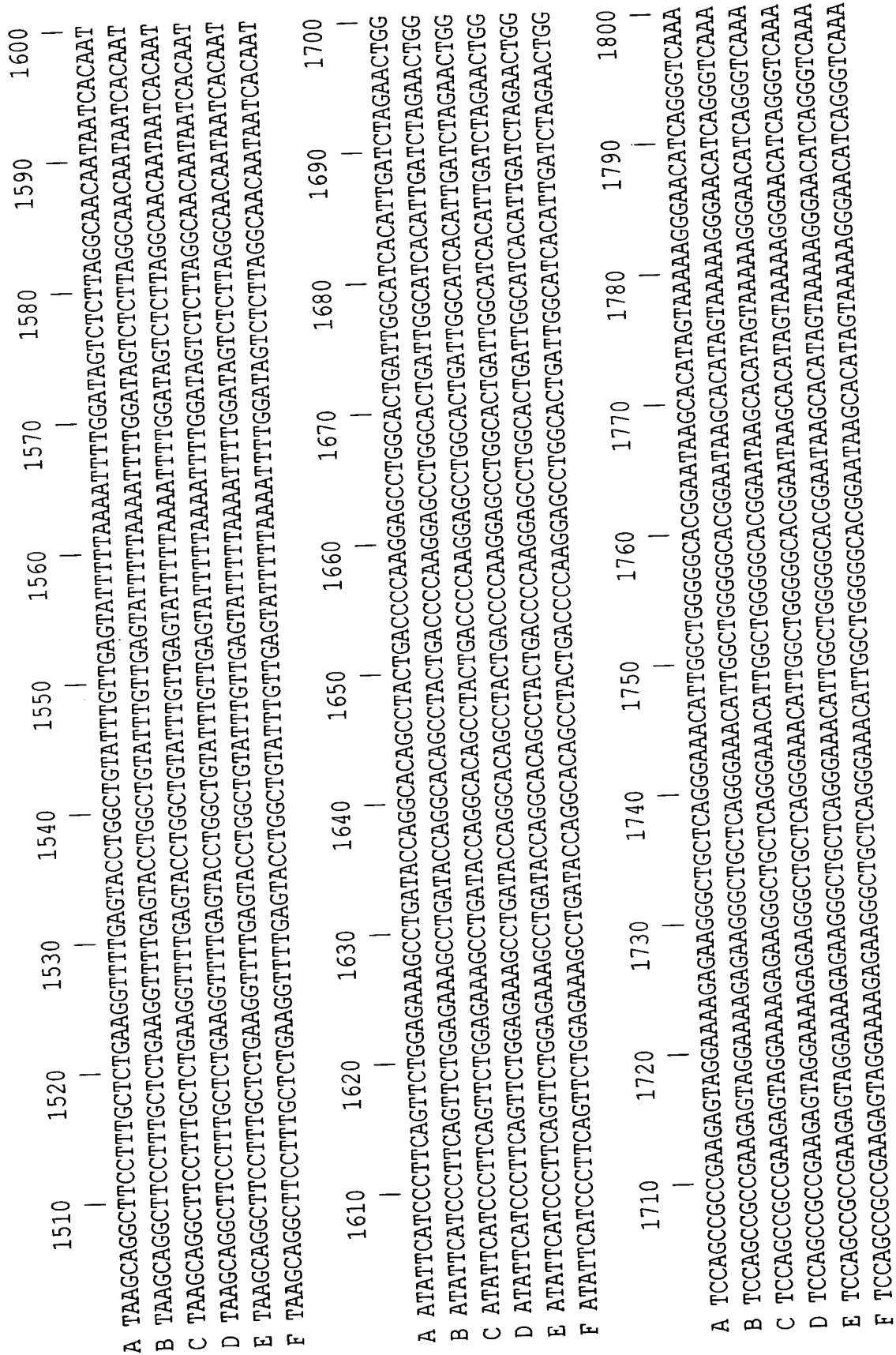


Fig. 11X-6

Figure 11X-8

2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
A	ATGTATACCAACAAGATTGTTGTAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTTGGCTCCTTAGCATG								
B	ATGTATACCAACAAGATTGTTGTAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTTGGCTCCTTAGCATG								
C	ATGTATACCAACAAGATTGTTGTAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTTGGCTCCTTAGCATG								
D	ATGTATACCAACAAGATTGTTGTAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTTGGCTCCTTAGCATG								
E	ATGTATACCAACAAGATTGTTGTAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTTGGCTCCTTAGCATG								
F	ATGTATACCAACAAGATTGTTGTAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTTGGCTCCTTAGCATG								
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
A	GCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTTTGAGATGGGGTGGAAATT								
B	GCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTTTGAGATGGGGTGGAAATT								
C	GCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTTTGAGATGGGGTGGAAATT								
D	GCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTTTGAGATGGGGTGGAAATT								
E	GCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTTTGAGATGGGGTGGAAATT								
F	GCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTTTGAGATGGGGTGGAAATT								
2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
A	GGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTGGAAAGGATAAGTGTCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
B	GGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTGGAAAGGATAAGTGTCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
C	GGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTGGAAAGGATAAGTGTCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
D	GGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTGGAAAGGATAAGTGTCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
E	GGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTGGAAAGGATAAGTGTCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
F	GGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTGGAAAGGATAAGTGTCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								

Fig. 11X-8

Figure 11X-9

	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	
A	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
B	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
C	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
D	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
E	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
F	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT										
	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	
A	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCCTTTAGTAGACAGTTTAATTTCCCCCA										
B	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCCTTTAGTAGACAGTTTAATTTCCCCCA										
C	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCCTTTAGTAGACAGTTTAATTTCCCCCA										
D	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCCTTTAGTAGACAGTTTAATTTCCCCCA										
E	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCCTTTAGTAGACAGTTTAATTTCCCCCA										
F	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCCTTTAGTAGACAGTTTAATTTCCCCCA										
	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	
A	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGTGGGAGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCA										
B	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGTGGGAGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCA										
C	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGTGGGAGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCA										
D	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGTGGGAGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCA										
E	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGTGGGAGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCA										
F	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGTGGGAGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCA										

Fig. 11X-9

"BFB" REFSeq

	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
A	TCATTGGGAGAGTTCC	TGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
B	TCATTGGGAGAGTTCC	TGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
C	TCATTGGGAGAGTTCC	TGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
D	TCATTGGGAGAGTTCC	TGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
E	TCATTGGGAGAGTTCC	TGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
F	TCATTGGGAGAGTTCC	TGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
A	CAAGCCACTGAATTTG	AGTTTTTTCACCTTGTGTTTCTAAATATGCTGTGTGAATCAGTACAGTTTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAA								
B	CAAGCCACTGAATTTG	AGTTTTTTCACCTTGTGTTTCTAAATATGCTGTGTGAATCAGTACAGTTTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAA								
C	CAAGCCACTGAATTTG	AGTTTTTTCACCTTGTGTTTCTAAATATGCTGTGTGAATCAGTACAGTTTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAA								
D	CAAGCCACTGAATTTG	AGTTTTTTCACCTTGTGTTTCTAAATATGCTGTGTGAATCAGTACAGTTTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAA								
E	CAAGCCACTGAATTTG	AGTTTTTTCACCTTGTGTTTCTAAATATGCTGTGTGAATCAGTACAGTTTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAA								
F	CAAGCCACTGAATTTG	AGTTTTTTCACCTTGTGTTTCTAAATATGCTGTGTGAATCAGTACAGTTTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAA								
	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
A	TGGGGTAGTAATACCT	ATCTCAAAAAAATTATTGACACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
B	TGGGGTAGTAATACCT	ATCTCAAAAAAATTATTGACACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
C	TGGGGTAGTAATACCT	ATCTCAAAAAAATTATTGACACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
D	TGGGGTAGTAATACCT	ATCTCAAAAAAATTATTGACACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
E	TGGGGTAGTAATACCT	ATCTCAAAAAAATTATTGACACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
F	TGGGGTAGTAATACCT	ATCTCAAAAAAATTATTGACACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								

**Fig. 11X-10**





Figure 11X-12

3310	3320	3330	3340	3350	3360	3370	3380	3390	3400
A	CTAAGCACAAAAATAAAAACTTATC	ACTGTAAAAA	AAAAAAAAA	AAAAAGTCTCTCGTATAGCA	AAAAATCTAACTGATGCAATCTCCATCTGGCCTTC				
B	CTAAGCACAAAAATAAAAACTTATC	ACTGTAAAAA	AAAAAAAAA	AAAAAGTCTCTCGTATAGCA	AAAAATCTAACTGATGCAATCTCCATCTGGCCTTC				
C	CTAAGCACAAAAATAAAAACTTATC	ACTGTAAAAA	AAAAAAAAA	AAAAAGTCTCTCGTATAGCA	AAAAATCTAACTGATGCAATCTCCATCTGGCCTTC				
D	CTAAGCACAAAAATAAAAACTTATC	ACTGTAAAAA	AAAAAAAAA	AAAAAGTCTCTCGTATAGCA	AAAAATCTAACTGATGCAATCTCCATCTGGCCTTC				
E	CTAAGCACAAAAATAAAAACTTATC	ACTGTAAAAA	AAAAAAAAA	AAAAAGTCTCTCGTATAGCA	AAAAATCTAACTGATGCAATCTCCATCTGGCCTTC				
F	CTAAGCACAAAAATAAAAACTTATC	ACTGTAAAAA	AAAAAAAAA	AAAAAGTCTCTCGTATAGCA	AAAAATCTAACTGATGCAATCTCCATCTGGCCTTC				
3410	3420	3430	3440	3450	3460	3470	3480	3490	3500
A	ATCCTTCTCCCTTTATTTGTCCTTT	TCGTGATTTGTTTCATCCAGCAAC	CCAGGATGATCTTGT	TAAACATTAACAGATTCTGT	CAYKCTTTMAAAAAA				
B	ATCCTTCTCCCTTTATTTGTCCTTT	TCGTGATTTGTTTCATCCAGCAAC	CCAGGATGATCTTGT	TAAACATTAACAGATTCTGT	CAYKCTTTMAAAAAA				
C	ATCCTTCTCCCTTTATTTGTCCTTT	TCGTGATTTGTTTCATCCAGCAAC	CCAGGATGATCTTGT	TAAACATTAACAGATTCTGT	CAYKCTTTMAAAAAA				
D	ATCCTTCTCCCTTTATTTGTCCTTT	TCGTGATTTGTTTCATCCAGCAAC	CCAGGATGATCTTGT	TAAACATTAACAGATTCTGT	CAYKCTTTMAAAAAA				
E	ATCCTTCTCCCTTTATTTGTCCTTT	TCGTGATTTGTTTCATCCAGCAAC	CCAGGATGATCTTGT	TAAACATTAACAGATTCTGT	CAYKCTTTMAAAAAA				
F	ATCCTTCTCCCTTTATTTGTCCTTT	TCGTGATTTGTTTCATCCAGCAAC	CCAGGATGATCTTGT	TAAACATTAACAGATTCTGT	CAYKCTTTMAAAAAA				
3510	3520	3530	3540	3550	3560	3570	3580	3590	3600
A	AAAGCCATGAAATNTAGCAAGCCAC	TGAATTTGAGTTTTTCACTTTT	CGTGTGTAATCAGANCAGKTTT	CTTACCCCTTTCTTGGTCTT					
B	AAAGCCATG-AAATNTAGCAAGCCAC	TGAATTTGAGTTTTTCACTTTT	CGTGTGTAATCAGANCAGKTTT	CTTACCCCTTTCTTGGTCTT					
C	AAAGCCATGAAATNTAGCAAGCCAC	TGAATTTGAGTTTTTCACTTTT	CGTGTGTAATCAGANCAGKTTT	CTTACCCCTTTCTTGGTCTT					
D	AAAGCCATGAAATNTAGCAAGCCAC	TGAATTTGAGTTTTTCACTTTT	CGTGTGTAATCAGANCAGKTTT	CTTACCCCTTTCTTGGTCTT					
E	AAAGCCATGAAATNTAGCAAGCCAC	TGAATTTGAGTTTTTCACTTTT	CGTGTGTAATCAGANCAGKTTT	CTTACCCCTTTCTTGGTCTT					
F	AAAGCCATGAAATNTAGCAAGCCAC	TGAATTTGAGTTTTTCACTTTT	CGTGTGTAATCAGANCAGKTTT	CTTACCCCTTTCTTGGTCTT					

Fig. 11X-12

	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700
A	AATTCCTTACTGATAAAATGGGGTGWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCATTAGACATT									
B	AATTCCTTACTGATAAAATGGGGTGWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCATTAGACATT									
C	AATTCCTTACTGATAAAATGGGGTGWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCATTAGACATT									
D	AATTCCTTACTGATAAAATGGGGTGWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCATTAGACATT									
E	AATTCCTTACTGATAAAATGGGGTGWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCATTAGACATT									
F	AATTCCTTACTGATAAAATGGGGTGWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCATTAGACATT									
	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800
A	AGGAGAAGCATTTTGTGGAGGATTGAAGTTGAGATCTTCCATCCAAAGTAGCTTTTCAATTGSTAGAAGCTTAATGTAGGCAAGCCACCTTCATTTT									
B	AGGAGAAGCATTTTGTGGAGGATTGAAGTTGAGATCTTCCATCCAAAGTAGCTTTTCAATTGSTAGAAGCTTAATGTAGGCAAGCCACCTTCATTTT									
C	AGGAGAAGCATTTTGTGGAGGATTGAAGTTGAGATCTTCCATCCAAAGTAGCTTTTCAATTGSTAGAAGCTTAATGTAGGCAAGCCACCTTCATTTT									
D	AGGAGAAGCATTTTGTGGAGGATTGAAGTTGAGATCTTCCATCCAAAGTAGCTTTTCAATTGSTAGAAGCTTAATGTAGGCAAGCCACCTTCATTTT									
E	AGGAGAAGCATTTTGTGGAGGATTGAAGTTGAGATCTTCCATCCAAAGTAGCTTTTCAATTGSTAGAAGCTTAATGTAGGCAAGCCACCTTCATTTT									
F	AGGAGAAGCATTTTGTGGAGGATTGAAGTTGAGATCTTCCATCCAAAGTAGCTTTTCAATTGSTAGAAGCTTAATGTAGGCAAGCCACCTTCATTTT									
	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900
A	CAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAAGA									
B	CAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAAGA									
C	CAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAAGA									
D	CAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAAGA									
E	CAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAAGA									
F	CAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAAGA									

Fig. 11X-13

	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000
A	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGAAACAAATCCACCTGAGATCAGCAGAGCCA									
B	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGAAACAAATCCACCTGAGATCAGCAGAGCCA									
C	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGAAACAAATCCACCTGAGATCAGCAGAGCCA									
D	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGAAACAAATCCACCTGAGATCAGCAGAGCCA									
E	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGAAACAAATCCACCTGAGATCAGCAGAGCCA									
F	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGAAACAAATCCACCTGAGATCAGCAGAGCCA									
	4010	4020	4030	4040	4050	4060	4070	4080	4090	
A	CCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGCACCTGCCCGGGCGGGCGCCCC									
B	CCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGCACCTGCCCGGGCGGGCGCCCC									
C	CCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGCACCTGCCCGGGCGGGCGCCCC									
D	CCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGCACCTGCCCGGGCGGGCGCCCC									
E	CCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGCACCTGCCCGGGCGGGCGCCCC									
F	CCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGCACCTGCCCGGGCGGGCGCCCC									

Fig. 11X-14

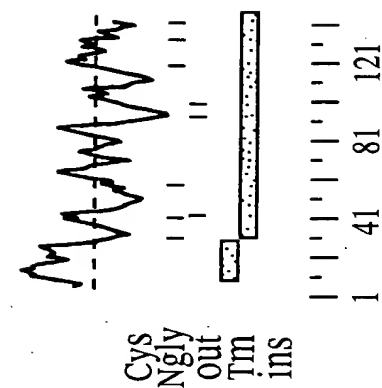


FIG. 11Y-1

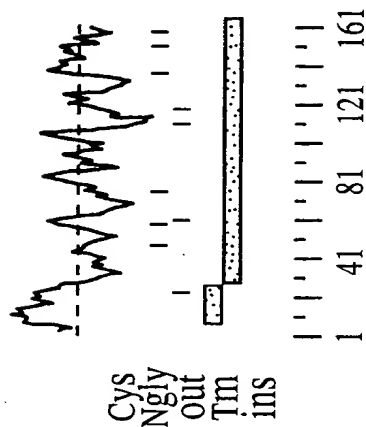


FIG. 11Y-3

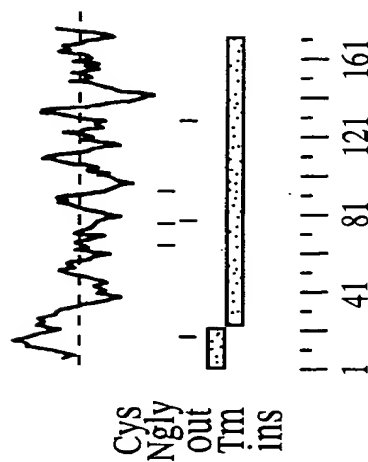


FIG. 11Y-2

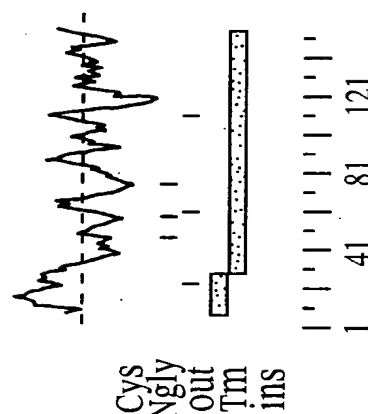


FIG. 11Y-4

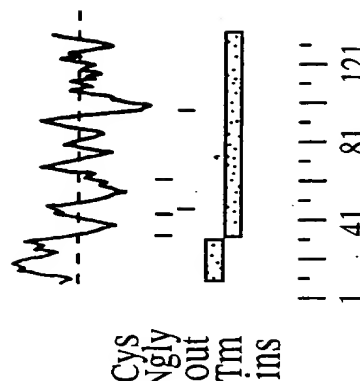


FIG. 11Y-5

FIG. 11Y-6

Figure 11Z-1

GTCGACCCAC	GGTCCGGTT	TGCTTGGAGA	TGCTGCTAAA	ACAGAGAGGC	TGTGAACAAG	60		
GACATTACCG	AGCAGGAGCA	TACATTACAGA	AGACAAGGAG	CCCTGCTCGC	TGCACCCGAAT	120		
ATCTTATCAA	AAAGACTCCT	ATCTGTATGC	CAACCCAGAC	TTCCAGAAAG	AGATCAGATC	180		
CCTGAATCCC	CATCATC	ATG AAC	TGG CAC	ATG ATC	TCG GGG	CTT ATC	230	
Met Asn Trp His Met Ile Ser Gly Leu Ile								
1		5		10				
GTA GTA	GTG ATC	AAA GTT	GGA ATG	ACC TTT	TTT CTG	TAT TTC	278	
Val Val	Val Ile	Lys Val	Val Gly	Met Thr	Phe Phe	Leu Leu	Tyr Phe	
15		20		25				
CCA CAG	GTT TTT	GGC AAA	AGT AAT	GAT GGC	TTC GTC	CCC ACG	GAG AGC	326
Pro Gln	Val Phe	Gly Lys	Ser Ser	Asn Asp	Gly Phe	Val Pro	Thr Glu	Ser
30		35		40				
TAC GGA	ACC ACT	AGT AGT	CAG AAT	GTC TCA	CAG ATC	TTT GGG	AGA AAT	374
Tyr Gly	Thr Thr	Ser Val	Gln Asn	Val Ser	Gln Ile	Phe Gly	Arg Asn	
45		50		55				
GAC GAA	AGT ACC	ATG CCT	ACA AGG	AGC TAT	GGA ACA	GTC TGT	CCC AGA	422
Asp Glu	Ser Thr	Met Pro	Thr Thr	Arg Ser	Tyr Gly	Thr Val	Cys Pro	Arg
60		65		70		75		
AAC TGG	GAT TTT	CAC CAA	GGA AAA	TGC TTT	TTC TTC	TCC TTC	TCC GAA	470
Asn Trp	Asp Phe	His Gln	Gly Lys	Cys Phe	Phe Phe	Ser Phe	Ser Glu	
80		85		90				

Fig. 11Z-1

"OFF" DEFECTION

TCA CCT TGG AAA GAC AGC ATG GAT TAT TGT GCA ACA CAA GGA TCC ACA	518
Ser Pro Trp Lys Asp Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr	
95	105
100	
CTG GCA ATT GTC AAC ACT CCA GAG AAA CTG AAG TAT CTT CAG GAC ATA	566
Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Lys Tyr Leu Gln Asp Ile	
110	120
115	
GCT GGT ATT GAG AAT TAC TTT ATT GGT TTG GTA CGT CAG CCT GGA GAG	614
Ala Gly Ile Glu Asn Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu	
125	135
130	
AAA AAG TGG CGC TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC	662
Lys Lys Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr	
140	150
145	155
AAT CAG GAC CAG AAC TTC GAC TGT GTC ACT ATA GGT CTG ACG AAG ACA	710
Asn Gln Asp Gln Asn Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr	
160	170
165	
TAT GAT GCT GCA TCA TGT GAA GTC AGC TAT CGC TGG ATC TGC GAA ATG	758
Tyr Asp Ala Ala Ser Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met	
175	185
180	

**Fig. 11Z-2**

AAT GCC AAA TGATCATAGA TCTCTACAAG AGTGAATTTT TACAGAGCTA	807
Asn Ala Lys	
190	
GCAAAGGAGA TTAGTTGTGA CTGAAACCAG CCCAGGAAAT ATAGAGCATC AAAGACTGTG	867
CCCATCTTCC ATAGGTGGAG TTCCCTATTG AATCCTCAAA GTCAATTTGT TACTCCACAA	927
ACATCTTCAC ATAGTAAAC TCCCTTTCTG ACCAAGTATT CCCTAAGACC ACAC TTCCTG	987
TGAGAGGGA CTGGATTCTA GTTATCTGCA GACAGAGCCA GGATTCTGGA GATGAAATCA	1047
ATATGGAAAT GCAGTCTGTT TCTGTAGAGC TGAGCCCTTTT AACTAATCAG TAGGGTTTGT	1107
TCTGTTGTCA GAACTGTTTG ATCCTTAGAG AACATGCCCA CGCCACTGAG GAGAAACTGC	1167
TCGTGGAACA GATATGAGAA CTGTTAGGAA GCACTATGGG CAGAAGAATA TAAACTTGGC	1227
TTCACAACAT CCCCATTCC AGAAAGCCTC CCATTCCCAT ACAACATCGT AGAAGCAGAG	1287
GTCCCTTCTGA ATTGGGGAAG GACCTCTACA GCTCGACTTG GTACTGAACA AATATTGAGG	1347
GAATGAAGAA AGTCTCTGAAT AGGACAGAGA TAAACAAGGA GGAGAAGGAA AGAGATAGGA	1407
AGAAAGGAGA AGTGGGAAGG AGGGGAAAA GGAATGATGG GCAGGAGAAA AAGAGACAGG	1467
AGCAGCCAGG AAAAACACTC AAGCTAAAAT TTTTTCAGGT TTTGGATAAA ATCTATTGTG	1527
ACATAAATAA TATCTTTTCA TTAGAAGAGA AAAGGCAAAA TTGGGGACAA ATGGGCACCA	1587
TGAGAGATGA AGCAGAGGTT AATTGATCA CAAGGAAAGA AAGGCAGGAA TGAGGTTGAA	1647
AACTTTTGG ATACCTTGGC TGTTATCTCA AGAAGGTACA AGCTGCATAA AGTATAGGAG	1707
AAAAGAGATG TGCTGGTTGT TTAAAGTAGC AAAAATTAAA CTACAGAGAA GCCTATAGAA	1767
AGCTAAAGGA ATTAAAACCA TCCAATAATC AATTCAATTAT TTTCAACTAA TAGCAATATG	1827
TATGTGCATT ACTAGTCAAA ATAAATTGTG AATTCTGTTA TTATAAAAAA AAAAAAAG	1887
GGCGGCCGC	1896

Fig. 11Z-3





MI289	ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTCAAAAGTTGTTGGAATG	60
HI289	ATGAACTGGCACATGATCATCTCGGGCTTATCGTAGTAGTCAAAAGTTGTTGGAATG	60
MI289	ACCTTTTCTGCTGTATTTCCACACAGGTTTTTGGCAAAAGTAATGATGGCTTCGTCCCC	120
HI289	ACCTTATTCTACTTTATTTCCACACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACC	120
MI289	ACGGAGAGCTACGGAACCACTAGTGTGCAGAAATGTCTCACAGATCTTTGGGAGAAATGAC	180
HI289	ACCGAGAGCTATGGAACA-----GTCTCACAGATTTTGGGAGCAGTTCCTCCCAAGTCCC	174
MI289	GAAAGTACCATGCCCTACAAGGAGCTATGGAACAGTCTGTCTCCAGAAACTGGGATTTTCAC	240
HI289	AACGGCTTCATTACCAACAAGGAGCTATGGAACAGTCTGCCCCCAAGACTGGGAAATTTAT	234
MI289	CAAGGAAAAATGCTTTTCTCTCTCTCTCCGAATCACCTTGGAAGACAGCATGGATTAT	300
HI289	CAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGGAAATGAAAGCAGGGACTTT	294

Fig. 11Z-4

. . . . .  
MI289 TGTGCAACACAAGGATCCACACTGGCAATTGTCAACACTCCAGAGAAACTGAAGTATCTT 360  
|| | ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||  
HI289 TGCAAAGGAAAAGGATCCACATTTGGCAATTGTCAACACGCCAGAGAAACTGAAGTTTCTT 354

. . . . .  
MI289 CAGGACATAAGCTGGTATTGAGAATTACTTTATTGGTTTGCTACGTCAGCCTGGAGAGAAA 420  
||||||| ||| | ||||||| ||||||| || || | ||||||| ||||  
HI289 CAGGACATAAAGCTGATGCTGAGAAAGTATTTTATTGGCTTAATTACCATCGTGAAGAGAAA 414

. . . . .  
MI289 AAGTGGCGCTGGATCAACAACCTCTGTGTTCAATGGCAATGTTACCAATCAGGACCAGAAC 480  
| ||||| ||||||| ||||||| ||||||| ||||||| || |||||  
HI289 AGTGGCGTTGGATCAACAACCTCTGTGTTCAATGGCAATGTTACATCATCCAATCAGAAT 474

. . . . .  
MI289 TTCGACTGTGTCACCTATAGGTCTGACGAAGACATATGATGCTGCATCATGTGAAGTCAGC 540  
| | | | | | | | | | ||| | | | | | |||||  
HI289 CAGAAATTTCAACTGTGCGACCAATTGGCCCTAACAAAAAGACATTTGATGCTGGTGACATCAGC 534

. . . . .  
MI289 TATCGCTGGATCTGCGAAATGAATGCCAAA 570  
|| ||| ||||||| || | ||||||| |||||  
HI289 TACCGCAGGATCTGTGAGAAGAATGCCAAA 564

**Fig. 11Z-5**

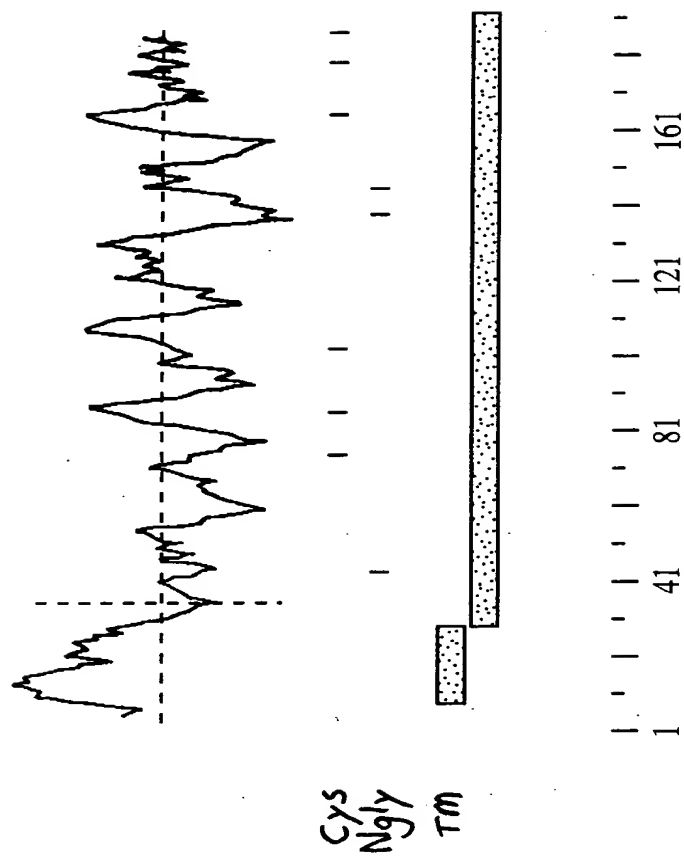


FIG. 11Z-6

L	F	L	G	G	V	G	M	V	G	T	V	A	V	T	V	M	P	Q	19
G	CTG	TTT	CTT	GGT	GGT	GGA	ATG	GTG	GGC	ACA	GTG	GCT	GTC	ACT	GTC	ATG	CCT	CAG	58
W	R	V	S	A	F	I	E	N	N	I	V	V	F	E	N	F	W	E	39
TGG	AGA	GTG	TCG	GCC	TTC	ATT	GAA	AAC	AAC	ATC	GTG	GTT	TTT	GAA	AAC	TTC	TGG	GAA	118
L	W	M	N	C	V	R	Q	A	N	I	R	M	Q	C	K	I	Y	D	59
CTG	TGG	ATG	AAT	TGC	GTG	AGG	CAG	GCT	AAC	ATC	AGG	ATG	CAG	TGC	AAA	ATC	TAT	GAT	178
L	L	A	L	S	P	D	L	Q	A	A	R	G	L	M	C	A	A	S	79
CTG	CTG	GCT	CTT	TCT	CCG	GAC	CTA	CAG	GCA	GCC	AGA	GGA	CTG	ATG	TGT	GCT	GCT	TCC	238
M	S	F	L	A	F	M	M	A	I	L	G	M	K	C	T	R	C	T	99
ATG	TCC	TTC	TTG	GCT	TTC	ATG	ATG	GCC	ATC	CTT	GGC	ATG	AAA	TGC	ACC	AGG	TGC	ACG	298
D	N	E	K	V	K	A	H	I	L	L	T	A	G	I	I	F	I	I	119
GAC	AAT	GAG	AAG	GTG	AAG	GCT	CAC	ATT	CTG	CTG	ACG	GCT	GGA	ATC	ATC	TTC	ATC	ATC	358
G	M	V	V	L	I	P	V	S	W	V	A	N	A	I	I	R	D	F	139
GGC	ATG	GTG	GTG	CTC	ATC	CCT	GTG	AGC	TGG	GTT	GCC	AAT	GCC	ATC	ATC	AGA	GAT	TTC	418
N	S	I	V	N	V	A	Q	K	R	E	L	G	E	A	L	Y	L	G	159
AAC	TCA	ATA	GTG	AAT	GTT	GCC	CAA	AAA	CGT	GAG	CTT	GGA	GAA	GCT	CTC	TAC	TTA	GGA	478

104/361

Fig. 12A

[illegible]

**Fig. 12B**

CCAAAAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCA	1676
TTTTTGTCTGTGAAAAATAAATTTCCTTCTTGTACCATTTCTGTGTTTACTAAAAATCTGTAAATACTGTATTTT	1755
TCTGTTTATTCCTCAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGT	1834
GTTCTATTTGCTTTATACATTTATTAATAAATTGTACATTTTCTAAAAAATAAAAAAATAAAAAAATAAAAAA	1909

**Fig. 12C**

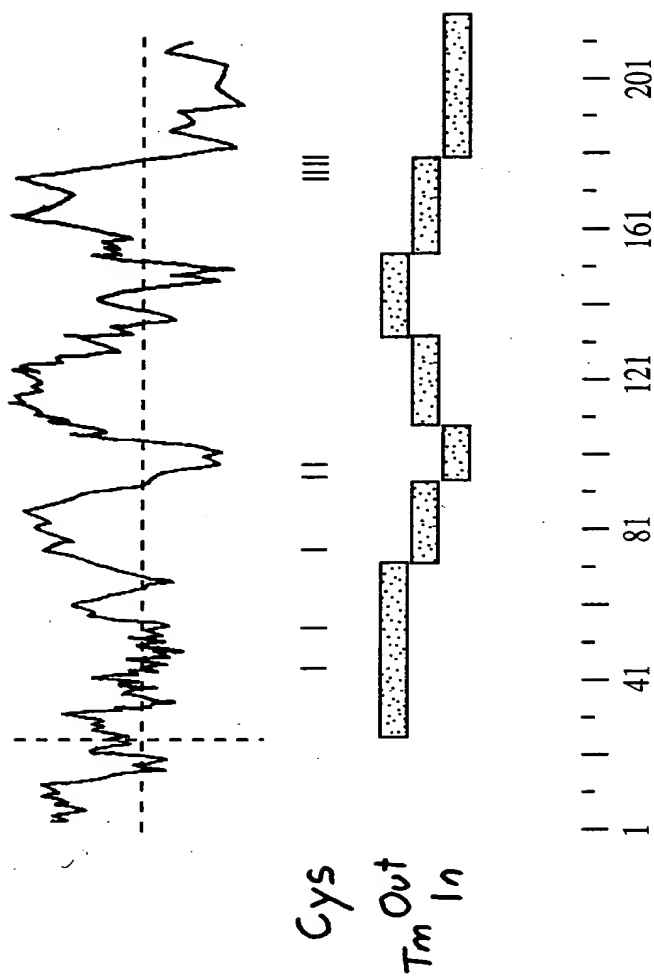


FIG. 12D

```

DKFZ G-----GGCA-----
:
:      ::::
I309 GCTGTTCTTGGTGTGTGGAATGGTGGGCACACAGTGGCTGTCACCTGATGCCCTCAGTGGAGAGTGTCG
      10      20      30      40      50      60      70

DKFZ -----

I309 GCCTTCATTGAAAACAACATCGTGGTTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCCGTGAGGC
      80      90      100     110     120     130     140

DKFZ -----

I309 AGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGC
      150     160     170     180     190     200     210

DKFZ -----

I309 CAGAGGACTGATGTGTGCTGCCGTCCGTGATGTCCTTCTTGGCTTTCATGATGCCCATCCTTGGCATGAAA
      220     230     240     250     260     270     280

DKFZ -----

I309 TGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCA
      290     300     310     320     330     340     350

```

Fig. 12E



DKFZ -----

I309 TCATCACGGGCATGGTGGTCTCATCCCTGTGAGCTGGGTGCGCAATGCCATCATCAGAGATTTCATAA  
360 370 380 390 400 410 420

DKFZ -----

I309 CTCAATAGTGAATGTTGCCCAAAAACGTGAGCTTGGAGAAAGCTCTCTACTTAGGATGGACCACGGCACTG  
430 440 450 460 470 480 490

DKFZ -----

I309 GTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAGAGCAGTAGCTACAGAT  
500 510 520 530 540 550 560

DKFZ -----

I309 ACTCGATACCTTCCCATCGCACAAACCCAAAAAGTTATCACACCGGAAAGAGTCACCGAGCGTCTACTC  
570 580 590 600 610 620 630

DKFZ -----

I309 CAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCATGCAAAATGACAAAAATC  
640 650 660 670 680 690 700

**Fig. 12F**



170	180	190	200	210	220	230
DKFZ	ACATAGATGAGTGTAACATTTATATCTCACATAGACATGCTTATATGCTTTTATTAAAAATGAAATGCG					
	::					
II309	ACATAGATGAGTGTAACATTTATATCTCACATAGACATGCTTATATGCTTTTATTAAAAATGAAATGCG					
990	1000	1010	1020	1030	1040	1050
240	250	260	270	280	290	300
DKFZ	CAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGTTGAAGAA					
	::					
II309	CAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGTTGAAGAA					
1060	1070	1080	1090	1100	1110	1120
310	320	330	340	350	360	370
DKFZ	GGTACTATTAAATTGTTTTAAAAACAGCTTAGGGATTAATGTCTCCATTATAATGAAGATTAAAAATGA					
	::					
II309	GGTACTATTAAATTGTTT-AAAAACAGCTTAGGGATTAATGTCTCCATTATAATGAAGATTAAAAATGA					
1130	1140	1150	1160	1170	1180	
380	390	400	410	420	430	440
DKFZ	AGGCTTTAATCAGCATTTGTAAAGGAAAATTGAAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAG					
	::					
II309	AGGCTTTAATCAGCATTTGTAAAGGAAAATTGAAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAG					
1190	1200	1210	1220	1230	1240	1250

**Fig. 12H**

**Fig. 12I**

```

730      740      750      760      770      780      790
DKFZ AGGTTTCATCAATATAATAAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAACAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AGGTTTCATCAATATAATAAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAACAA
1540      1550      1560      1570      1580      1590      1600

      800      810      820      830      840      850      860
DKFZ CAACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 CAACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTT
1610      1620      1630      1640      1650      1660      1670

      870      880      890      900      910      920      930
DKFZ TTGTTCTGGAATAATAATTTCCTTCTTGTAACCATTTCTGTTAGTTTACTAAAAATCTGTAAATCTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 TTGTTCTGGAATAATAATTTCCTTCTTGTAACCATTTCTGTTAGTTTACTAAAAATCTGTAAATCTG
1680      1690      1700      1710      1720      1730      1740

      940      950      960      970      980      990      1000
DKFZ TATTTTCTGTTTATTCCAAATTTGATGAAACTGACAAATCCAATTTGAAAGTTTGTGTCGACGTCGTCT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 TATTTTCTGTTTATTCCAAATTTGATGAAACTGACAAATCCAATTTGAAAGTTTGTGTCGACGTCGTCT
1750      1760      1770      1780      1790      1800      1810

```

Fig. 12J

```

1010      1020      1030      1040      1050      1060      1070
DKFZ AGCTTAAATGAATGTGTTCTATTGCTTTTATACATTTATATAATAAATTGTACATTTTTCCTCAAAAAAAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AGCTTAAATGAATGTGTTCTATTGCTTTTATACATTTATATAATAAATTGTACATTTTTCCTCAAAAAAAA
1820      1830      1840      1850      1860      1870      1880

1080      1090
DKFZ AAAAAAAAAA-----
      ::::::::::::
I309 AAAAAAAAAAAAAAAAAAAAAA
1890      1900

```

Fig. 12K

I309	G-----CTGTTTCTTGGTGGTGTGAATGGTGGCACAGTGGCTG .: : :::::::::::::::::::: : CLAUD8 ATGGCAACCTACGCTCTTCAAATGGCTGCACTGGTGCTTGGTGGTGTGGCATGGTGGGCACGGTGGCTG 10    20    30    40    50    60    70
I309	TCACTGTCA TGCCTCAGTGGAGAGTGTCGGCCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACTTCTG : :::::::::::::::::::: : .::: : : : : : : : : : : : CLAUD8 TGACTATCATGCCCTCAGTGGAGAGTGCTCGCCTTCATCGAAAAGTAACATTGTGGTGTGTGAGAACC GCTG 80     90    100    110    120    130    140
I309	GGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAATACTATGATTC C CTG : :::::::::::::: : : :::::::::::::::::::: : : : : : : : : : : CLAUD8 GGAAGGCTTGTGGATGAATTGTATGAGGCATGCCA ACATCAGAATGCAGTGCAAAGGCTACGACTCCCCTG 150    160    170    180    190    200    210
I309	CTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGT CCTTCTTGG : :::::::::: CLAUD8 CTGGCTCTTAGTCCAGACCTCCAGGCATCCCAGGACTGATGTGTGCTGCCGTCCGCTCTTGGCTTTCTTGG 220    230    240    250    260    270    280

**Fig. 12L**

	260	270	280	290	300	310	320
I309	CTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAAGGTGAAGGCTCA						
	.....	.....	.....	.....	.....	.....	.....
CLAUD8	CTTTCATGACAGCCATCCTCGGAATGAAGTGCAACAGATGCACGGGGACGATGAGAACGTGAAGAGCCG						
	290	300	310	320	330	340	350
	330	340	350	360	370	380	390
I309	CATTCTGCTGACGGCTGGAATCATCTTTCATCATCACGGGCATGGTGGTCTCATCCCCTGTGAGCTGGGTT						
	::: .....	.....	.....	.....	.....	.....	.....
CLAUD8	CATCTTGCTGACAGCCGGAATCATCTTCTTCATCACCGGCTTGGTTGTGCTCATCCCCTGTGAGCTGGGTT						
	360	370	380	390	400	410	420
	400	410	420	430	440	450	460
I309	GCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAATGTGCCCAAAAACGTGAGCTTGAGAAG						
	.....	.....	.....	.....	.....	.....	.....
CLAUD8	GCCAATTCCATCATCAGAGACTTCTACAACCCACTGGTGGATGTGGCCCTAAAGCCGAGCTGGGAGAAG						
	430	440	450	460	470	480	490
	470	480	490	500	510	520	530
I309	CTCTCTACTTAGGATGGACCAACGGCACTGGTGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTG						
	:	.....	.....	.....	.....	.....	.....
CLAUD8	CCCTCTACATAGGCTGGACCAACAGCGCTGGTGTGCTGATCGCTGGAGGAGCACTGTTCTGTGTGTTTTTG						
	500	510	520	530	540	550	560

Fig. 12M



	540	550	560	570	580	590	600
I309	TTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATACTTCCCATCGCACAAACCCAAAAAGTTATCAC						
	:::	:::	:::	:::	:::	:::	:::
CLAUD8	TTGTAAGAAAGGAGCAACAGTTACAGGTAACCGTACCATCCCATCGCACCACTCAACGGAGTTTCCAC						
	570	580	590	600	610	620	630
	610	620	630	640	650	660	670
I309	ACCGGAAAGAGTCACCGAGCGTCTACTCCAGAAAGTCAGTATGTGTATGTTTTTAACTTT						
	.....	.....	.....	.....	.....	.....	.....
CLAUD8	GCCGAAAAGAGATCTCCGAGCATATACTCCAAAAGTCAGTATGTGTAG-----						
	640	650	660	670			
	680	690	700	710	720	730	740
I309	ACTATAAGCCATGCAAAATGACAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAAACTTTGATT						
CLAUD8	-----						
	750	760	770	780	790	800	810
I309	TACTGTTCTTAACTGCCTAAATCTTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAAGCTATT						
CLAUD8	-----						

Fig. 12N

	820	830	840	850	860	870	880
I 309	TCAGCAGAA	TGAGATAT	TAAACCCAA	TGCTTTGATT	GTTCTAGAA	AGTATAGTA	ATTGTTTCTAAGGT
CLAUD8	-----						
	890	900	910	920	930	940	950
I 309	GGTCAAGCA	TCTACTCT	TTTTATCAT	TTTACTTCAA	AATGACATT	GCTAAAGAC	TGTCATTATTTACTAC
CLAUD8	-----						
	960	970	980	990	1000	1010	1020
I 309	TGTAATTT	CTCCACGA	CATAGCAT	TATGTACAT	AGATGAGTG	TAAACATT	TATATCTCACATAGACATG
CLAUD8	-----						
	1030	1040	1050	1060	1070	1080	1090
I 309	CTTATATG	GTTTATT	TAAATGAA	ATGCCAGT	CCATTACAC	TGTAATAA	TAGAACTCAACTATTGCTTT
CLAUD8	-----						
	1100	1110	1120	1130	1140	1150	1160
I 309	TCAGGAAAT	CATGGAT	AGGTTGA	AGAGGTTA	CTATTAA	TGTTTAA	AAAACAGCTTAGGATTAAATGT
CLAUD8	-----						

Fig. 120

# Sequence

```

1170      1180      1190      1200      1210      1220      1230
I 309 CCTCCATTATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTG
CLAUD8 -----

1240      1250      1260      1270      1280      1290      1300
I 309 ATATGCTGTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTT
CLAUD8 -----

1310      1320      1330      1340      1350      1360      1370
I 309 TTCTTGTTATTAATTAACATTTTAAAGAGCAGATATTTGTCAAGGGGCTTTCATTCAAACTGCTT
CLAUD8 -----

1380      1390      1400      1410      1420      1430      1440
I 309 TTCCAGGGCTATACTCAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTAGGAAAGTGAA
CLAUD8 -----

```

**Fig. 12P**

**Fig. 12Q**

CCF000000

1800 1810 1820 1830 1840 1850 1860  
I309 ATTTGAAAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTATATT

CLAUD8 -----

I309 AATAAATTGTACATTTTCTAAAAAATAAAAAAAAAAAAAA

CLAUD8 -----

Fig. 12R

CLAUD8	MATYALQMAALVLGGVGMVGTVAVTIMPQWRVSAFIESNIVVFENRWEGLWMNCMRHANIRMQCKVYDSL	10	20	30	40	50	60	70
I309	-----LFLGGVGMVGTVAVTIMPQWRVSAFIENNIIVVFENRWEGLWMNCVRQANIRMQCKIYDSL	10	20	30	40	50	60	
CLAUD8	LALSPDLQASRGLMCAASVLAFLAFMTAILGMKCTRCTGDDENVKSRILLTAGIIFITGLVVLIPVSWV	80	90	100	110	120	130	140
I309	LALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIPVSWV	70	80	90	100	110	120	130
CLAUD8	ANSIIRDFYNPLVDVALKRELGEALYIGWTTALVLIAGGALFCCVCCCTERSNSYRYSVPSHRTTQRSEH	150	160	170	180	190	200	210
I309	ANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGALFCCVCCNEKSSSYRYSIPSHRTTQKSYH	140	150	160	170	180	190	200
CLAUD8	AEKRSPSIYSKSQYV	220						
I309	TGKKSPSVYSRSQYV	210						

Fig. 12S

```

I309 .....LFLGGVMGTVAVTMPQWRVSAFIENNIVVFENFWEGL 40
hCPE MASMGLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIIVTSQTIWEGL 50
mCPE MASMGLQVLIGISLAVLGWLGIIILSCALPMWRVTAFIGSNIIVTAQTSWEGL 50
rRPV .MSMSLEITGTSLAVLGWLCTIVCCALPMWRVSAFIGSSIIITAQITWEGL 49

I309 WMNCVRQANIRMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAIL 90
hCPE WMNCVVQSTGQMCKVYDSSLALPQDLQAARALVISIIVAALGVLLSVV 100
mCPE WMNCVVQSTGQMCKMYDMLALPQDLQAARALMVISIIVGALGMLLSVV 100
rRPV .WMNCV.QSTGQMCKMYDSSLALPQDLQAARALIVVSILAAFGLLVALV 98

I309 GMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIPVSWVANAIIRD FYN 140
hCPE GGKCTNCLD.ESAKAKTMIIVAGVVFLLAGLMVIVPVSWTAHNI IQDFYN 149
mCPE GGKCTNCMED.ETVKAKIMITAGAVFIVASMLIMVPVSWTAHNVIRDFYN 149
rRPV GAQCTNCVQD.ETAKAKITIVAGVLFLLAAVLTLPVSVSANTIIIRD FYN 147

I309 SIVNVAQKRELGEALYLGWTTALVLI VGGALFCCVFCCKNEKSSSYRYSIP 190
hCPE PLVASGQKREMGASLYVGWAAAGLLLLGGGLLCC.NCPRTDKPYS AKYS 198
mCPE PMVASGQKREMGASLYVGWAAAGLLLLGGGLLCCSCPPRSNDKPYS AKYS 199
rRPV PLVPEAQKREMGTLGYVGWAAALQLLGGALLCCSCPPREKYAPT KILYS 197

I309 SHRTTQKSYHTGKKSPSVYSRSQYV 215
hCPE AARSAASNYV..... 209
mCPE AARSVPASNYV..... 210
rRPV APRSTGPGTGTAYDRKTTSERPGARTPHHHHYQPSMYPTRPACSLA SET 248

```

Fig. 12T

# Figure 13A

CGAGCGGCCCGCCGCGGTCAGACATGGGCCAAGGAGCCAGAGGCCGTCGCGGGTCTGTGAGTTGAGCTTGAGGCCG	79
<div>M R V I M G I A S L G F L W A V F L</div> <div>CAGG ATG AGG GTC ATC ATG GGG ATA GCC AGC CTG GGG TTC CTC TGG GCA GTA TTC CTG</div>	18 137
<div>L P L V F G V P T E E T T F G E S V A S</div> <div>CTT CCT CTT GTG TTT GGG GTC CCC ACA GAG GAG ACT ACC TTT GGA GAA TCT GTG GCC TCC</div>	38 197
<div>H L P K G C R R C C D P E D L M S S D D</div> <div>CAT CTC CCC AAA GGC TGT CGA CGA TGC TGT GAC CCC GAG GAC CTG ATG TCC TCT GAT GAT</div>	58 257
<div>T V Q A P V S P Y V L P E V R P Y L G R</div> <div>ACG GTC CAG GCC CCT GTT TCC CCT TAT GTC CTG CCT GAA GTC AGG CCG TAC CTC GGC CGC</div>	78 317
<div>D H</div> <div>GAC CAC</div>	80 323

124/361

Fig. 13A



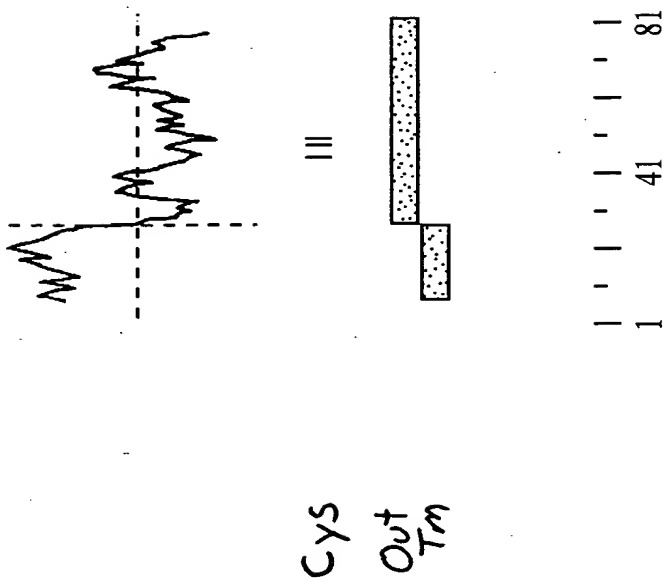


FIG. 13B

CGGACGCGTGGCGGACGCGTGGGTTATTCTTTGGTTAGGTATAATATGGGCATTTAAACACACCCAGTTT 79  
M E F L Y R I V V G F I L I F T 16  
TGTA CTGTGATAAGT ATG GAA TTC TTA TAT AGG ATT GTT GGT GGA TTC ATT CTT ATC TTT ACA 142  
F F N I K G Q N T K C P M S C Y Y I V R 36  
TTT TTT AAT ATT AAG GGA CAG AAT ACC AAG TGT CCA ATG TCT TGT TAT TAT ATT GTT AGG 202  
V L G T L G I L T V F W V C P L T I F N 56  
GTA CTG GGC ACT TTG GGG ATA TTG ACT GTA TTC TGG GTT TGC CCC CTC ACT ATT TTT AAT 262  
P D Y F I P I S I T I V L T L L G I L 76  
CCA GAC TAT TTT ATA CCT ATC AGT ATA ACT ATA GTT CTT ACT CTT CTT CTT GGA ATT CTT 322  
F L I V Y Y G S F H P N R S A E T K C D 96  
TTT CTT ATT GTT TAT TAT GGG AGT TTT CAC CCA AAC AGA AGT GCA GAA ACA AAA TGT GAT 382  
E I D G K P V L R E C R M R Y F L M E \* 115  
GAA ATT GAT GGA AAA CCA GTT CTA AGA GAA TGT AGA ATG AGA TAT TTC CTA ATG GAA TAA 442  
GCTATTCATTATGATATATATTTCTTATATTTTGTTCATTGGTTAGTAAAGAAATGTGTGTTAAAAA 521  
AAAAA 546

Fig. 14A

DEPTO DE FISIOL

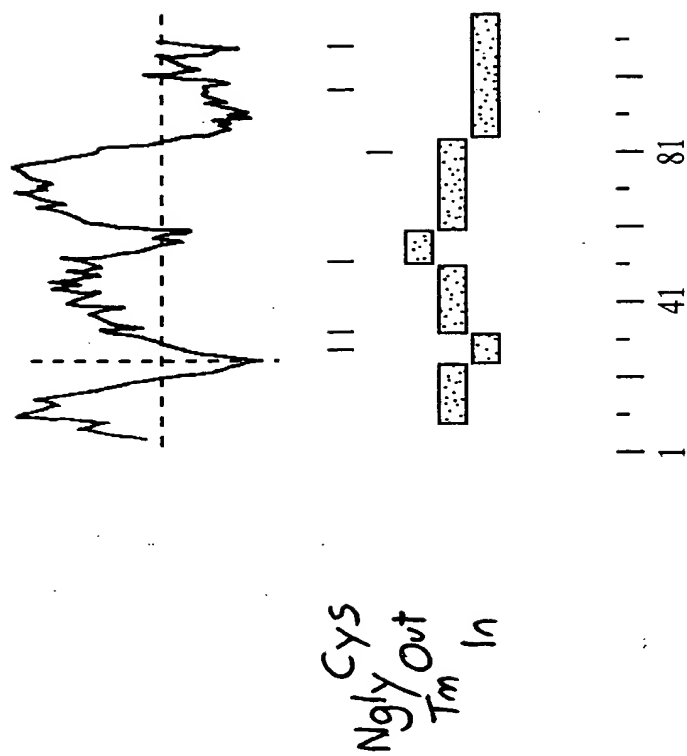


FIG. 14B



# 129/361

I	S	K	G	I	A	D	I	M	I	A	F	R	T	R	V	H	G	R	C	168
ATT	TCA	AAG	GGG	ATT	GCA	GAC	ATC	ATG	ATT	GCC	TTT	AGG	ACT	CGA	GTC	CAT	GGT	CGG	TGT	548
P	R	Y	F	D	G	P	L	G	V	L	G	H	A	F	P	P	G	P	G	188
CCT	CGC	TAT	TTT	GAT	GGT	CCC	TTG	GGA	GTG	CTT	GGC	CAT	GCC	TTT	CCT	CCT	GGT	CCG	GGT	608
L	G	G	D	T	H	F	D	E	D	E	N	W	T	K	D	G	A	G	F	208
CTG	GGT	GGT	GAC	ACT	CAT	TTT	GAT	GAG	GAT	GAA	AAC	TGG	ACC	AAG	GAT	GGA	GCA	GGA	TTC	668
N	L	F	L	V	A	A	H	E	F	G	H	A	L	G	L	S	H	S	N	228
AAC	TTG	TTT	CTT	GTG	GCT	GCT	CAT	GAA	TTT	GGT	CAT	GCA	CTG	GGG	CTC	TCT	CAC	TCC	AAT	728
D	Q	T	A	L	M	F	P	N	Y	V	S	L	D	P	R	K	Y	P	L	248
GAT	CAA	ACA	GCC	TTG	ATG	TTC	CCA	AAT	TAT	GTC	TCC	CTG	GAT	CCC	AGA	AAA	TAC	CCA	CTT	788
S	Q	D	D	I	N	G	I	Q	S	I	Y	G	G	L	P	K	V	P	A	268
TCT	CAG	GAT	GAT	ATC	AAT	GGA	ATC	CAG	TCC	ATC	TAT	GGA	GGT	CTG	CCT	AAG	GTA	CCT	GCT	848
K	P	K	E	P	T	I	P	H	A	C	D	P	D	L	T	F	D	A	I	288
AAG	CCA	AAG	GAA	CCC	ACT	ATA	CCC	CAT	GCC	TGT	GAC	CCT	GAC	TTG	ACT	TTT	GAC	GCT	ATC	908
T	T	F	R	R	E	V	M	F	F	K	G	R	H	L	W	R	I	Y	Y	308
ACA	ACT	TTC	CGC	AGA	GAA	GTA	ATG	TTC	TTT	AAA	GGC	AGG	CAC	CTA	TGG	AGG	ATC	TAT	TAT	968

Fig. 15B

D I T D V E F E L I A S F W P S L P A D 328  
 GAT ATC ACG GAT GTT GAG TTT GAA TTA ATT GCT TCA TTC TGG CCA TCT CTG CCA GCT GAT 1028  
  
 L Q A A Y E N P R D K I L V F K D E N F 348  
 CTG CAA GCT GCA TAC GAG AAC CCC AGA GAT AAG ATT CTG GTT TTT AAA GAT GAA AAC TTC 1088  
  
 W M I R G Y A V L P D Y P K S I H T L G 368  
 TGG ATG ATC AGA GGA TAT GCT GTC TTG CCA GAT TAT CCC AAA TCC ATC CAT ACA TTA GGT 1148  
  
 F P G R V K K I D A A V C D K T T R K T 388  
 TTT CCA GGA CGT GTG AAG AAA ATA GAT GCA GCC GTC TGT GAT AAG ACC ACA AGA AAA ACC 1208  
  
 Y F F V G I W C W R F D E M T Q T M D K 408  
 TAC TTC TTT GTG GGC ATT TGG TGC TGG AGG TTT GAT GAA ATG ACC CAA ACC ATG GAC AAA 1268  
  
 G F P Q R V V K H F P G I S I R V D A A 428  
 GGA TTC CCG CAG AGA GTG GTA AAA CAC TTT CCT GGA ATC AGT ATC CGT GTT GAT GCT GCT 1328  
  
 F Q Y K G G F F F S R G S K Q F E Y N I 448  
 TTC CAG TAC AAA GGA TTC TTC TTT TTC AGC CGT GGA TCA AAG CAA TTT GAA TAC AAC ATT 1388  
  
 K T K N I T R I M R T N T W F Q C K E P 468  
 AAG ACA AAG AAT ATT ACC CGA ATC ATG AGA ACT AAT ACT TGG TTT CAA TGC AAA GAA CCA 1448

Fig. 15C

# SEQUENCE

K	N	S	S	F	G	F	D	I	N	K	E	K	A	H	S	G	G	I	K	488
AAG	AAC	TCC	TCA	TTT	GGT	TTT	GAT	ATC	AAC	AAG	GAA	AAA	GCA	CAT	TCA	GGA	GGC	ATA	AAG	1508
I	L	Y	H	K	S	L	S	L	F	I	F	G	I	V	H	L	L	K	N	508
ATA	TTG	TAT	CAT	AAG	AGT	TTA	AGC	TTG	TTT	ATT	TTT	GGT	ATT	GTT	CAT	TTG	CTG	AAA	AAC	1568
T	S	I	Y	Q	*															514
ACT	TCT	ATT	TAT	CAA	TAA															1586
ATTCATAGACCTAAATAAACCTCAACAGGTCCTTTTAATATAAATTCTGCTTCAAAAATAGAAATAAAACCATTCCTTAAC																				1665
AACAAAAAATAAAAAA																				1684

131/361

Fig. 15D

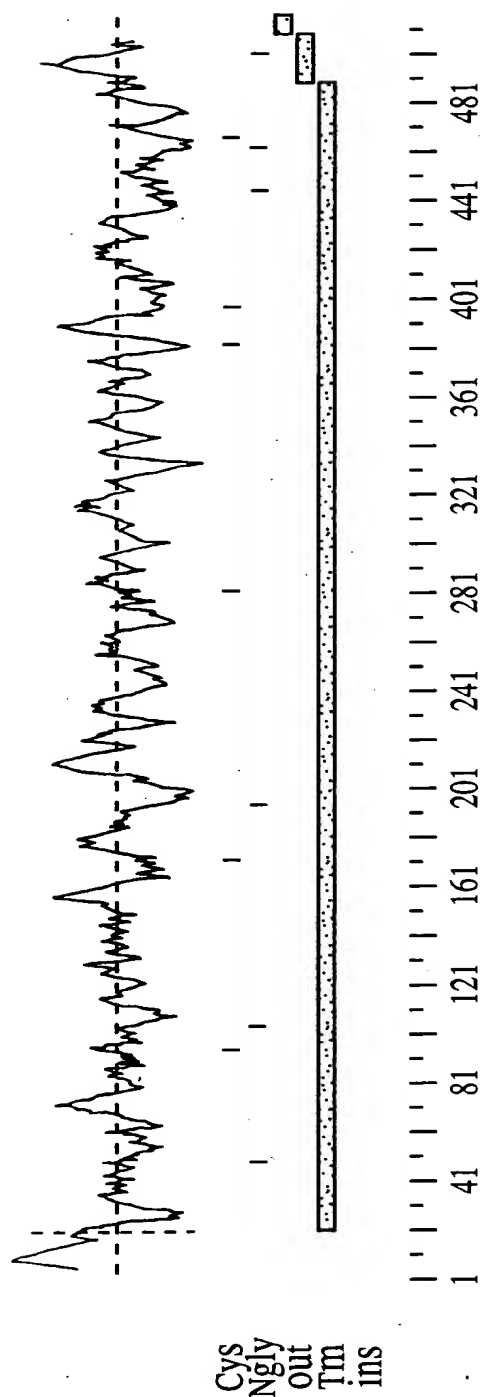


FIG. 15E



# FIGURE 15F

GCTTTAACTGAAGAGACAGGA																				ATG	AAG	TGC	CTT	CTG	TCT	CTG	ATG	GTT	AAT	TTT	ATA	ACA	13			
																																60				
L	S	A	A	F	P	P	D	R	K	D	K	N	E	E	N	N	Q	L	A	33																
CTT TCC GCT GCA TTT CCT CCA GAC AGG AAG GAC AAA AAT GAG GAG AAC AAC CAA CTG GCC																				120																
Q	A	Y	L	N	Q	F	Y	S	L	E	I	E	G	S	H	F	V	Q	S	53																
CAG GCA TAT CTC AAC CAG TTC TAC TAC TCT CTT GAA ATA GAA GGG AGT CAT TTT GTC CAA AGC																				180																
K	N	R	S	L	F	D	G	K	L	R	E	M	Q	A	F	F	G	L	T	73																
AAG AAC AGG AGT CTC TTT GAT GGA AAA CTT CGG GAA ATG CAG GCA TTT TTC GGA TTG ACA																				240																
																																				133/361
V	T	G	K	L	D	S	D	T	L	A	I	M	K	V	P	R	C	G	V	93																
GTG ACT GGA AAA CTG GAT TCA GAC ACA CTT GCG ATC ATG AAA GTG CCC AGG TGT GGG GTA																				300																
P	D	V	G	Q	Y	G	Y	T	L	P	G	W	R	K	Y	S	L	T	Y	113																
CCA GAT GTG GGG CAA TAT GGC TAC ACA CTC CCT GGG TGG AGA AAA TAC AGC CTT ACA TAC																				360																
R	I	M	N	Y	T	P	D	M	T	P	A	D	V	D	E	A	I	Q	K	133																
AGA ATA ATG AAC TAT ACT CCT GAT ATG ACA CCA GCT GAT GTG GAT GAG GCT ATT CAG AAA																				420																
A	L	Q	V	W	S	K	V	T	P	L	T	F	T	R	I	S	K	G	V	153																
GCT CTA CAA GTT TGG AGC AAG GTC ACT ACT CCA CTG ACG TTT ACC AGG ATA TCC AAG GGG GTT																				480																

Fig. 15F

# Table 10

A	D	I	M	I	A	F	R	T	G	V	H	G	W	C	P	R	H	F	D	173
GCA	GAT	ATA	ATG	ATA	GCA	TTC	AGG	ACA	GGA	GTC	CAT	GGC	TGG	TGT	CCT	CGT	CAC	TTT	GAT	540
G	P	L	G	V	L	G	H	A	F	P	P	G	L	G	L	G	G	D	T	193
GGT	CCT	CTG	GGA	GTC	CTT	GGC	CAT	GCC	TTT	CCT	CCT	GGT	CTG	GGT	CTA	GGT	GGT	GAC	ACT	600
H	F	D	E	D	E	T	W	I	A	K	D	G	E	G	F	N	L	F	L	213
CAC	TTT	GAC	GAA	GAT	GAA	ACA	TGG	ATA	GCC	AAG	GAT	GGG	GAA	GGG	TTC	AAC	TTG	TTT	CTT	660
V	A	A	H	E	F	G	H	S	L	G	L	S	H	S	N	D	Q	T	A	233
GTG	GCT	GCT	CAT	GAA	TTT	GGT	CAC	TCT	CTG	GGG	CTG	TCC	CAC	TCC	AAT	GAT	CAA	ACA	GCC	720
L	M	F	P	N	Y	I	S	L	D	P	S	K	Y	P	L	S	Q	D	D	134/253
TTG	ATG	TTC	CCC	AAT	TAC	ATC	TCC	CTG	GAT	CCT	AGC	AAA	TAC	CCA	CTT	TCT	CAG	GAT	GAT	361/780
I	D	G	I	Q	S	I	Y	G	S	P	P	K	V	T	T	K	P	S	G	273
ATT	GAT	GGG	ATC	CAG	TCC	ATC	TAT	GGA	AGT	CCA	CCT	AAG	GTA	ACC	ACC	AAG	CCA	AGT	GGA	840
N	S	E	P	H	A	C	D	P	T	L	T	F	D	A	I	T	T	F	R	293
AAT	TCT	GAA	CCC	CAC	GCC	TGT	GAC	CCC	ACC	TTG	ACT	TTT	GAT	GCT	ATC	ACT	ACT	TTC	CGC	900
R	E	V	M	F	F	K	G	R												302
AGG	GAA	GTT	ATG	TTC	TTT	AAA	GGC	AGG												927

Fig. 15G

# GenBank

TAAACCTATCCCTTGACACTCCAGCTTCTTATAAAGATGTTTTTTTTTCAAGGATCTCCGGATAAACAGTCTTCTA 1007  
 CTCAGCTAGAAAGCCAGTTGCTGAGCATGTACCATGATCAGCAAGAGATTCTTCTCAAGAAACAATGTAGAAACAA 1087  
 TCAAAGAAAACACCCAAAGGCAACCTGCAGCTCCACACATAGCACACATGCAATTCACATGTATGCCCCACATATGTA 1167  
 ACATGTAGGCACACATGCATGCATACCAACCAAACTTAAGACTGAAACATGCTGATGGACACAGGTACCAGGACA 1247  
 TCATTGATGAAATATTTTGTGTTTAATGCAGG 1279  
  
 H L W R V Y S D I A G A E F E F I D S F 322  
 CAC TTA TGG AGG GTC TAC TCT GAT ATT GCT GGT GCT GAG TTT GAG TTT ATT GAT TCC TTC 1339  
  
 W P S L P A D L Q A A Y E S P R D E L L 342  
 TGG CCA TCT CTG CCA GCT GAT CTT CAA GCT GCC TAT GAA AGC CCC AGA GAT GAG CTC CTT 1399  
  
 V F K D E N F W V I R G Y S V L P G Y P 362  
 GTT TTT AAA GAT GAG AAT TTC TGG GTC ATC AGG GGA TAT TCT GTC TTG CCC GGT TAC CCC 1459  
  
 K S I H T L G F P R R V K K I D A A V C 382  
 AAA TCC ATC CAC ACA CTC GGA TTT CCA AGA CGT GTG AAG AAA ATT GAT GCA GCC GTC TGT 1519  
  
 D H D T R K T F F F V G I W C W R Y D E 402  
 GAT CAT GAT ACA AGA AAA ACC TTC TTT TTT GGT GGC ATC TGG TGC TGG AGG TAT GAT GAG 1579  
  
 M A Q A M D R G F P Q R I I K C F P G I 422  
 ATG GCA CAA GCA ATG GAC AGA GGA TTC CCA CAG AGG ATA ATA AAG TGC TTC CCA GGA ATT 1639

Fig. 15H

# Figure 15I

R	L	R	V	D	A	V	F	Q	H	N	G	F	L	Y	F	F	H	G	S	442
CGC	CTC	CGT	GTG	GAT	GCT	GTC	TTC	CAA	CAT	AAT	GGA	TTC	CTC	TAT	TTC	TTC	CAT	GGG	TCG	1699
R	Q	F	E	Y	D	M	K	A	K	N	I	T	Q	V	I	K	T	N	S	462
AGG	CAA	TTT	GAA	TAT	GAC	ATG	AAG	GCG	AAA	AAT	ATC	ACC	CAA	GTG	ATC	AAA	ACC	AAT	TCT	1759
W	F	L	C	N	E	P	L	N	A	S	F	N	V	S	V	K	G	K	A	482
TGG	TTC	CTG	TGT	AAC	GAA	CCA	TTA	AAC	GCA	TCA	TTC	AAT	GTC	AGT	GTC	AAA	GGA	AAA	GCA	1819
N	S	I	G	T	V	I	L	H	H	K	R	L	S	L	L	T	F	S	I	502
AAT	TCA	ATT	GGC	ACA	GTG	ATA	TTA	CAT	CAT	AAA	AGG	TTA	AGC	TTG	CTC	ACT	TTC	AGT	ATT	1879
V	H	V	L	T	K	T	Y	N	*											136/361
GTT	CAT	GTG	CTG	ACA	AAA	ACA	TAC	AAT	TAA	CAATAAA	TTCCACA	AAATAAA	ACC	AAACAA	AAATCTTT	TAACC				511
TGAACTCTGCCTCAGGAAGACTCAAGAGTGGGAGAGATGACCCAGTGGTTAAGTGCACTGGCTGCTCTTTCAAGGACCC	2029																			
AGGTTTGATTCAGTACCCACATGGCAGTCCACAGCTCTCTGTAACTCCAGACCCAGGAAATCTGATGCCCTCTCTGG	2109																			
CCTCTGAGGGCACTGCACAAGCATGGTGCCATAGACATATACATGCAAGCAACGGCTATATATTTAAAAATAAAATGAAAA	2189																			
AGTAAATAAATTGAGCCCAATTCTTTAGCATCAAGTTCCTACTACTATATATCAGCTGGGTAACCAATAACCAAGTTA	2269																			
AAGTATCTGATTCTTAACAGTGAAGTTTAAATATGACAAAAATCTCTCACTTATTTTGAGTCTAATTAATGATTGC	2349																			
AAACTTGGAATAATTAAAGCATGTCTTTAAAAATAAACATTAAGACAAATCTTAAATCCAAAAATAAAAAATAAAAA	2429																			
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2467																			

Fig. 15I



**Fig. 15K**

human	280	290	300	310	320	330	340
	PTIPHACDPDLTFDAIT	TFRRVMMFKGRHLWRI	YDITDVEFFELIASFW	PSLPADLQAAYENPRDK	ILV		
murine	280	290	300	310	320	330	340
	NSEPHACDPDLTFDAIT	TFRRVMMFKGRHLWRI	YSDIAGAEFFIDSWP	SLPADLQAAYESPRDEL	LV		
human	350	360	370	380	390	400	410
	FKDENFWMIRGYAVLP	DYPKSIHTLGFPGRV	KKIDAAVCDKTTTRK	TYFFVGIWCWRFDEMT	QTMDKGF	PQ	
murine	350	360	370	380	390	400	410
	FKDENFWVIRGYSVLP	GYPKSIHTLGFPRRV	KKIDAAVCDHDTRKT	FFFVGIWCWRYDEMAQ	AMDRGFP	PQ	
human	420	430	440	450	460	470	480
	RVVKHFPGISIRVDAA	FQYKGFFFSRSGSKQ	FEYNIKTKNITRIMRT	NWTFQCKEKNSSFG	FDINKEKA		
murine	420	430	440	450	460	470	480
	RIIKCFPGIRLRVDAV	FQHNGFLYFFHGSRQ	FEYDMKAKNITQVIK	TNSWFLCNEPLNASF	NVSV-KGKA		
human	490	500	510				
	HSGGIKILYHKSLSLF	IFGIVHLLKNTSIYQ					
murine	490	500	510				
	NSIGTVILHHKRLSLL	TFSIVHVLTKTYN					

Fig. 15L

# Sequence

```

human  CGGACGCGTGGCGGACGCGTGGCAGCTGAAGAAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTT 10      20      30      40      50      60      70
murine  -----GCTTT-----AACTGAAGA--GACAGGAATGAAGTGCCTTCTGTCTCTGATGGT 10      20      30      40

human  GTTCTTTATAACATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAATAATGAAGAAAATATGCAACTG 80      90      100     110     120     130     140
murine  TAATTTATAACACTTTCGCTGCAATTTCTCCAGACAGGAAGACAAAAATGAGGAGAACACCAACTG 80      90      100     110

human  GCTCAGGCATATCTCAACCCAGTTCTACTCTCTTGAAAATAGAAGGGAATCATCTTGTTCAAAGCAAGAATA 150     160     170     180     190     200     210
murine  GCCCAGGCATATCTCAACCCAGTTCTACTCTCTTGAAAATAGAAGGAGTCAATTTGTCCAAAGCAAGAACA 120     130     140     150     160     170     180

human  GGAGTCTCATAGATGACAAAATTTCGGGAAATGCAAGCATTTTGTGGATTGACAGTGACTGGAAAACCTGGA 220     230     240     250     260     270     280
murine  GGAGTCTCTTTGATGGAAAACCTTCGGGAAATGCAGGCATTTTTCGGATTGACAGTGACTGGAAAACCTGGA 190     200     210     220     230     240     250

```

**Fig. 15M**



**Fig. 15N**

**Fig. 150**

Figure 15P

```

840      850      860      870      880      890      900
human  AGGTACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCTGTGACCCCTGACTTGACTTTTGACGCTAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine  AGGTAACCAACCAAGCCAAGTGGAAATTCTGAACCCACGCTGTGACCCACCTTGACTTTTGATGCTAT
820      830      840      850      860      870      880

      910      920      930      940
human  CACAACCTTCCGCGAGAGAAATAATGTTCTTTAAAGGCAGG-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine  CACTACTTTCGCGAGGAAGTTATGTTCTTTAAAGGCAGGTAAACCTATTCCTTGACACTCCAGCTTCT
890      900      910      920      930      940      950

human  -----

murine  TATAAAGATGTTTTTTTTTTTCAAAAGGATCTCCGGATAAACAGTCTTCTACTCAGCTAGAAAGCCAGTTG
960      970      980      990      1000      1010      1020

human  -----

murine  CTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCCCTCAAGAAACAATGTAGAAAAACAATCAAAAGAAA
1030      1040      1050      1060      1070      1080      1090

```

Fig. 15P

**Fig. 15R**

**Fig. 15Q**

**Fig. 15Q**

1330	1340	1350	1360	1370	1380	1390	
human	GCTTCCAGTACAAAGGATTCTTCTTTT	CAGCCGTGGATCAAAGCAATT	TGAATACAAATTAAGACAA				
	:	.....	.....	.....	.....	.....	.....
murine	GTCTTCCAACATAATGGATTCTCTATT	CTTCCATGGTCGAGGCAATT	TGAATATGACATGAAGGCGA				
1660	1670	1680	1690	1700	1710	1720	
1400	1410	1420	1430	1440	1450	1460	
human	AGAATATTACCCGAATCATGAGAACTA	TACTTGGTTTCAATGCAAAAGAACT	CCTCATTTGG				
	:	.....	.....	.....	.....	.....	.....
murine	AAAATATCACCCAAAGTGATCAAAACCA	ATTCTTGGTTCCTGTGTAACGAACCA	TTAACGCATCATTCAA				
1730	1740	1750	1760	1770	1780	1790	
1470	1480	1490	1500	1510	1520	1530	
human	TTTTGATATCAACAAGGAAAAAGCACAT	TCAGGAGGCATAAAGATATT	TGTATCATAAGAGTTTAAGCTTG				
	:	.....	.....	.....	.....	.....	.....
murine	TGTCAGTGTCA--AAGGAAAAGCAAAT	TCAATTGGCACAGTGATATT	TACATCATATAAAGGTTAAGCTTG				
1800	1810	1820	1830	1840	1850	1860	
1540	1550	1560	1570	1580	1590	1600	
human	TTTATTTTGGTATTGTTCAATTGCTG	AAAAACACTTCTATTATCAATAAATC	-----ATAGACCTAA				
	:	.....	.....	.....	.....	.....	.....
murine	CTCACITTCAGTATTGTTTCATGTGCT	GACAAAAACATAACAATT	AACAATAAATTCACAAATAAACCCAAA				
1870	1880	1890	1900	1910	1920	1930	

Fig. 15S



```

human TAACAACA-----
      ::::::::::
murine TAGCATCAAGTTCTTACTCCTACTATATATCAGCTGGGTAACCAATAACCAAGTAAAGTATCTGATTCTT
      2220 2230 2240 2250 2260 2270 2280

human -----

murine CTAACAGTGAAGTTTAAATATGACAAAAATCTCTCACTTATTTTGAGTCTAATTAATGATTGCAAACT
      2290 2300 2310 2320 2330 2340 2350

human -----

murine TGGAAAATTAAAGCATGTCTTAAAAATAAACATTAAAGACAATTCTTAATCCAAAAAATAAAAAAA
      2360 2370 2380 2390 2400 2410 2420

human -----
      1680
      -----AAAAAATAAAAA
      ::::::::::::::
murine AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
      2430 2440 2450 2460
```

Fig. 15U



**Fig. 15V**



**Fig. 15X-1**

**Fig. 15X-2**

**Fig. 15X-3**



```

1100      1110      1120      1130      1140      1150      1160
210 TAGGTTTCCAGGACGTGTGAAGAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAACCTACTT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
MMP-8 ATGGCTTCCCAGCAGCGTCCAAGCAATTGACGCAGC-----TGTTTCTACAGAAGTAAACATACTT
      1110      1120      1130      1140      1150      1160

1170      1180      1190      1200      1210      1220      1230
210 CTTTGTGGGCATTGTGGTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGAGA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
MMP-8 CTTTGTAATGACCAATTCTGGAGATATGAT-----AACCAAAGACAATT-----CATGGAGC
      1170      1180      1190      1200      1210

1240      1250      1260      1270      1280      1290      1300
210 GTGGTAAACACCTTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGGATTCTTCTTTT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
MMP-8 CAGGT-----TATCCCAAAGCA-TATC-----AGGTGC--CTTTCAGGAATAGAGAGTAAA-----
      1220      1230      1240      1250      1260

1310      1320      1330      1340      1350      1360      1370
210 TCAGCCGTGGATCAAAGCAATTGGAATACAAACATTAAAGACAAAGAATATTACCCGAATCATGAGAACTAA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
MMP-8 -----GTTGAT-----GCAGTTT---TCCAGCA-----AGAACATTTC---TTC-----
      1270      1280      1290      1300

```

Fig. 15X-5

```

1380      1390      1400      1410      1420      1430      1440
210 TACTTGGTTTCAATGCAAAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAGGAAAAGCACAT
      :... : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 --CATG---TC--TTCAGTGGACCAAGATATTACGCATTTGATCTT-ATTGCT-CAGAGAGTTA-C-----
      1310      1320      1330      1340      1350

1450      1460      1470      1480      1490      1500      1510
210 TCAGGAGGCATAAAGATATTGTATCATAAAGAGTTTAAGCTTGTATTATTTTGGTATTGTTTCATTGCTGA
      :... :... :... :... :... :... :... :... :... :... :... :... :... :... :... :...
MMP-8 -CAGA-----GTTGCAAGAG-----GCA-----ATAAATGG-----C-TTAACTGT
      1360      1370      1380      1390

1520      1530
210 AAAACACTTCTATTATCAAA
      :... :... :
MMP-8 AGA-----TATGGC--
      1400

```

Fig. 15X-6



GAAAAGCGCTGGCCGAGGGCCCGGGCCCGGGGTGAGCGTGCCGAGCGGCTGTGGCGCAGGCTTCCAGCC	79
M P W P L L L L L A V S G A Q T T R	18
CCCACC ATG CCG TGG CCC CTG CTG CTG CTG GGC GTG AGT GGG GCC CAG ACA ACC CGG	139
P C F P G C Q C E V E T F G L F D S F S	38
CCA TGC TTC CCC GGG TGC CAA TGC GAG GTG GAG ACC TTC GGC CTT TTC GAC AGC TTC AGC	199
L T R V D C S G L G P H I M P V P I P L	58
CTG ACT CGG GTG GAT TGT AGC GGC CTG GGC CCC CAC ATC ATG CCG GTG CCC ATC CCT CTG	259
D T A H L D L S S N R L E M V N E S V L	78
GAC ACA GCC CAC TTG GAC CTG TCC AAC CGG CTG GAG ATG GTG AAT GAG TCG GTG TTG	319
A G P G Y T T L A G L D L S H N L L T S	98
GCG GGG CCG GGC TAC ACG ACG TTG GCT GGC CTG GAT CTC AGC CAC AAC CTG CTC ACC AGC	379
I S P T A F S R L R Y L E S L D L S H N	118
ATC TCA CCC ACT GCC TTC TCC CGC CTT CGC TAC CTG GAG TCG CTT GAC CTC AGC CAC AAT	439
G L T A L P A E S F T S S P L S D V N L	138
GGC CTG ACA GCC CTG CCA GCC GAG AGC TTC ACC AGC TCA CCC CTG AGC GAC GTG AAC CTT	499

Fig. 16A

S	H	N	Q	L	R	E	V	S	V	S	A	F	T	T	H	S	Q	G	R	158
AGC	CAC	AAC	CAG	CTC	CGG	GAG	GTC	TCA	GTG	TCT	GCC	TTC	ACG	ACG	CAC	AGT	CAG	GGC	CGG	559
A	L	H	V	D	L	S	H	N	L	I	H	R	L	V	P	H	P	T	R	178
GCA	CTA	CAC	GTG	GAC	CTC	TCC	CAC	AAC	CTC	ATT	CAC	CGC	CTC	GTG	CCC	CAC	CCC	ACG	AGG	619
A	G	L	P	A	P	T	I	Q	S	L	N	L	A	W	N	R	L	H	A	198
GCC	GGC	CTG	CCT	GGC	CCC	ACC	ATT	CAG	AGC	CTG	AAC	CTG	GCC	TGG	AAC	CGG	CTC	CAT	GCC	679
V	P	N	L	R	D	L	P	L	R	Y	L	S	L	D	G	N	P	L	A	218
GTG	CCC	AAC	CTC	CGA	GAC	TTG	CCC	CTG	CGC	TAC	CTG	AGC	CTG	GAT	GGG	AAC	CCT	CTA	GCT	739
V	I	G	P	G	A	F	A	G	L	G	G	L	T	H	L	S	L	A	S	238
GTC	ATT	GGT	CCG	GGT	GCC	TTC	GCG	GGG	CTG	GGA	GGC	CTT	ACA	CAC	CTG	TCT	CTG	GCC	AGC	799
L	Q	R	L	P	E	L	A	P	S	G	F	R	E	L	P	G	L	Q	V	258
CTG	CAG	AGG	CTC	CCT	GAG	CTG	GCG	CCC	AGT	GGC	TTC	CGT	GAG	CTA	CCG	GGC	CTG	CAG	GTC	859
L	D	L	S	G	N	P	K	L	N	W	A	G	A	E	V	F	S	G	L	278
CTG	GAC	CTG	TCG	GGC	AAC	CCC	AAG	CTT	AAC	TGG	GCA	GGA	GCT	GAG	GTG	TTT	TCA	GGC	CTG	919
S	S	L	Q	E	L	D	L	S	G	T	N	L	V	P	L	P	E	A	L	298
AGC	TCC	CTG	CAG	GAG	CTG	GAC	CTT	TCG	GGC	ACC	AAC	CTG	GTG	CCC	CTG	CCT	GAG	GCG	CTG	979

Fig. 16B

L L H L P A L Q S V S V G Q D V R C R R 318  
 CTC CTC CAC CTC CCG GCA CTG CAG AGC GTC AGC GTG GGC CAG GAT GTG CGG TGC CGG CGC 1039  
  
 L V R E G T Y P R R P G S S P K V A L H 338  
 CTG GTG CGG GAG GGC ACC TAC CCC CGG AGG CCT GGC TCC AGC CCC AAG GTG GCC CTG CAC 1099  
  
 C V D T R E S A A R G P T I L \* 354  
 TGC GTA GAC ACC CGG GAA TCT GCT GCC AGG GGC CCC ACC ATC TTG TGA 1147  
  
 CAAATGTTGGCCACAGACTGCTGTCTGGCTGCTCAGGTCCCGAGTAACCTATGTTCAATGTG 1226  
 CCAACACAGGGGAGCCCGCAGGCTATGTGGCAGCGTCACACAGGAGTTGTGGCCCTAGGAGAGGCTTTGGACCT 1305  
 GGGAGCCACACCTAGGAGCAAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGC 1384  
 CAAACAGACTCGGGTCCCCCTCTGCTTCCCCCTTATCCCCCAAGTGCCCTTCCCTCATGCTGGGCCGCCCTG 1463  
 ACCCGCAATGGGCAGAGGTGGGTGGGACCCCTGCTGCAGGGCAGAGTTCAAGTCCACTGGGCTGAGTGTCCCCCTTGG 1542  
 GCCCATGGCCCACTCAGGGCGAGTTTCTTTCTAACATAGCCCTTCTTTGCCATGAGGCCCATGAGGCCCGCTT 1621  
 CATCCTTTTCTATTTCCCTAGAACCTTAATGTAGAGGAATTGCAAGAATCAAGTCCACCCCTTCTCATGTGACAGAT 1700  
 GGGAAACTGAGGCCCTTGAGAAAGGAAAGGCTAATCTAAGTTCTCTAATAAGCCCCACCCCTCCCGCTGGCTCCCTTGCTGC 1779  
 GCCTCCAGCCCGACCCCAATGCACCTTTCTGTCTCTAATAAGCCCCACCCCTCCCGCTGGCTCCCTTGCTGC 1858  
 CCTTGCCTGTTCCCATTTAGCACAGGAGTAGCAGCAGGACAGGCAAGAGCCTCACAAAGTGGGACTCTGGGCCCTCTG 1937  
 ACCAGCTGTGGGCATGGGCTAAGTCACTCTGCCCCTTCGGAGCCCTCTGGAAGCTTAGGGCACATTTGGTTCCAGCCCTAGC 2016  
 CAGTTTCTCACCCCTGGGTGGGTCCCCCAGCATCCAGACTGGAAACCTACCCATTTTCCCTGAGCATCCTCTAGATG 2095  
 CTGCCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCATCTGGCTGGATCTCCAAGGGCCCTCCTGGATTCAAGTCCCCACT 2174  
 GGCCCTGAGCACGACAGCCCTTCTTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATG 2253

Fig. 16C

CTCTACCCAGGCGAGCATCTCAGCTTCCGAACCCCTGGGCTGTTTCTTAGTCTTTCATTTTATAAAAGTTGTGCTT 2332  
 TTTAACGGAGTGTCACCTTTCAACCGGCTTCCCCTACCCCTGCTGCCGGGATGGAGACATGTCAATTGTAAAGCAGA 2411  
 AAAAGTTGCATTTGTTCACCTTTTGTAATATTGTCCTGGCCCTGTGTTGGGTGTTGGGGAAGCTGGGCATCAGTGGC 2490  
 CACATGGGCATCAGGGGCTGGCCCCACAGAGACCCCAAGGCAGTGAGCTCTGTCTTCCCCCACCTGCTAGCCCCATC 2569  
 ATCTATCTAACCGGTCCTTGATTTAATAAACACTATAAAAGTTAAAAAATAAAAAA 2628

Fig. 16D

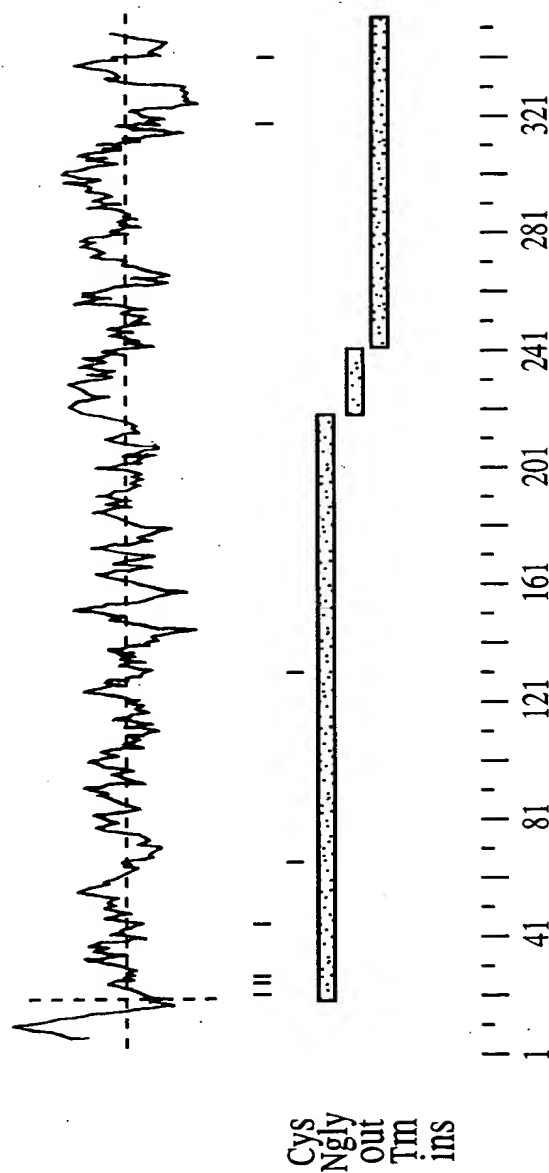


FIG. 16E

GTCGACCCACGGTCCGCCCGCCTAGCGCCGGGTCGGCCGAGCCGAGCCGAGCGGAGCCGGCGGAGCCTC 79  
 TGGAAATCACCCGGTCCGTGTTCTGAGGTGTCAGGTGACAGGGCGGTGGTGATGGCGCAGTTTGACACTGAAT 158  
 ACCAGCGCCTAGAGGCCTCCTATAGTGAATTCACCCAGGGAGGAGCACCTGTTGGTGACGTCGCCGAGGGAGCAA 237  
 GTCACCTTGGCACCATATTGAAAACCTTGACCTCTTCTCTCGAGTTTATAATCTGCACCAGAAATGGCTTCACA 316

M L I G E I F E L M Q F L F V V A F T 19  
 TGT ATG CTC ATC GGG GAG ATC TTT GAG CTC ATG CAG TTC CTC TTT GTG GTT GCC TTC ACT 376

T F L V S C V D Y D I L F A N K M V N H 39  
 ACC TTC CTG GTC AGC TGC GTG GAC TAT GAC ATC CTA TTT GCC AAC AAG ATG GTG AAC CAC 436

S L H P T E P V K V T L P D A F L P A Q 59  
 AGT CTT CAC CCT ACT GAA CCC GTC AAG GTC ACT CTG CCA GAC GCC TTT TTG CCT GCT CAA 162/361 496

V C S A R I Q E N G S L I T I L V I A G 79  
 GTC TGT AGT GCC AGG ATT CAG GAA AAT GGC TCC CTT ATC ACC ATC CTG GTC ATT GCT GGT 556

V F W I H R L I K F I Y N I C C Y W E I 99  
 GTC TTC TGG ATC CAC CGG CTT ATC AAG TTC ATC TAT AAC ATT TGC TGC TAC TGG GAG ATC 616

H S F Y L H A L R I P M S A L P Y C T W 119  
 CAC TCC TTC TAC CTG CAC GCT CTG CGC ATC CCT ATG TCT GCC CTT CCG TAT TGC ACG TGG 676

Fig. 17A

Q E V Q A R I V Q T Q K E H Q I C I H K 139  
CAA GAA GTG CAG GCC CGG ATC GTG CAG ACG CAG AAG GAG CAC CAG ATC TGC ATC CAC AAA 736

R E L T E L D I Y H R I L R F Q N Y M V 159  
CGT GAG CTG ACA GAA CTG GAC ATC TAC CAC CGC ATC CTC CGT TTC CAG AAC TAC ATG GTG 796

A L V N K S L L L P L R F R L P G L G E A 179  
GCA CTG GTT AAC AAA TCC CTC CTG CCT CTG CGC TTC CGC CTG CCT GGC CTC GGC GAA GCT 856

V F F T R G L K Y N F E L I L F W G P G 199  
GTC TTC TTC ACC CGT GGT CTC AAG TAC AAC TTT GAG CTG ATC CTC TTC TGG GGA CCT GGC 916

S L F L N E W S L K A E Y K R G Q R L 219  
TCT CTG TTT CTC AAT GAA TGG AGC CTC AAG GCC GAG TAC AAA CGT GGC GGC CAA CGG CTA 976

E L A Q R L S N R I L W I G I A N F L L 239  
GAG CTG GCC CAG CGC CTC AGC AAC CGC ATC CTG TGG ATT GGC ATC GCT AAC TTC CTG CTG 1036

C P L I L I W Q I L Y A F F S Y A E V L 259  
TGC CCC CTC ATC CTC ATA TGG CAA ATC CTC TAT GCC TTC TTC AGC TAT GCT GAG GTG CTG 1096

K R E P G A L G A R C W S L Y G R C Y L 279  
AAG CGG GAG CCG GGC GCC CTC GGA GCA CGC TGC TGG TCA CTC TAT GGC CGC TGC TAC CTC 1156

Fig. 17B

R	H	F	N	E	L	E	H	E	L	Q	S	R	L	N	R	G	Y	K	P	299
CGC	CAC	TTC	AAC	GAG	CTG	GAG	CAC	GAG	CTG	CAG	TCC	CGC	CTC	AAC	CGT	GGC	TAC	AAG	CCC	1216
A	S	K	Y	M	N	C	F	L	S	P	L	L	T	L	L	A	K	N	G	319
GCC	TCC	AAG	TAC	ATG	AAT	TGC	TTC	TTG	TCA	CCT	CTT	TTG	ACA	CTG	CTG	GCC	AAG	AAT	GGA	1276
A	F	F	A	G	S	I	L	A	V	L	I	A	L	T	I	Y	D	E	D	339
GCC	TTC	TTC	GCT	GGC	TCC	ATC	CTG	GCT	GTG	CTT	ATT	GCC	CTC	ACC	ATT	TAT	GAC	GAA	GAT	1336
V	L	A	V	E	H	V	L	T	T	V	T	L	L	G	V	T	V	T	V	359
GTG	TTG	GCT	GTG	GAA	CAT	GTG	CTG	ACC	ACC	GTC	ACA	CTC	CTG	GGG	GTC	ACC	GTG	ACC	GTG	1396
C	R	S	F	I	P	D	Q	H	M	V	F	C	P	E	Q	L	L	R	V	379
TGC	AGG	TCC	TTT	ATC	CCG	GAC	CAG	CAC	ATG	GTG	TTT	TGC	CCT	GAG	CAG	CTG	CTC	CGC	GTG	1456
I	L	A	H	I	H	Y	M	P	D	H	W	Q	G	N	A	H	R	S	Q	399
ATC	CTC	GCT	CAC	ATC	CAC	TAC	ATG	CCT	GAC	CAC	TGG	CAG	GGT	AAT	GCC	CAC	CGC	TCG	CAG	1516
T	R	D	E	F	A	Q	L	F	Q	Y	K	A	V	F	I	L	E	E	L	419
ACC	CGG	GAC	GAG	TTT	GCC	CAG	CTC	TTC	CAG	TAC	AAG	GCA	GTG	TTC	ATT	TTG	GAA	GAG	TTG	1576
L	S	P	I	V	T	P	L	I	L	I	F	C	L	R	P	R	A	L	E	439
CTG	AGC	CCC	ATT	GTC	ACA	CCC	CTC	ATC	CTC	ATC	TTC	TGC	CTG	CGC	CCA	CGG	GCC	CTG	GAG	1636

Fig. 17C



I	I	D	F	F	R	N	F	T	V	E	V	G	V	G	D	T	C	S	459	
ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	1696
F	A	Q	M	D	V	R	Q	H	G	H	P	Q	W	L	S	A	G	Q	T	479
TTT	GCT	CAG	ATG	GAT	GTT	CGC	CAG	CAT	GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	1756
E	A	S	V	Y	Q	Q	A	E	D	G	K	T	E	L	S	L	M	H	F	499
GAG	GCC	TCA	GTG	TAC	CAG	CAA	GCT	GAG	GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	1816
A	I	T	N	P	G	W	Q	P	P	R	E	S	T	A	F	L	G	F	L	519
GCC	ATC	ACC	AAC	CCT	GGC	TGG	CAG	CCA	CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTC	CTC	1876
K	E	Q	V	Q	R	D	G	A	A	A	S	L	A	Q	G	G	L	L	P	539
AAG	GAG	CAG	GTT	CAG	CGG	GAT	GGA	GCA	GCT	GCT	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT	1936
E	N	A	L	F	T	S	I	Q	S	L	Q	S	E	S	E	P	L	S	L	559
GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT	1996
I	A	N	V	V	A	G	S	S	C	R	G	P	P	L	P	R	D	L	Q	579
ATC	GCA	AAT	GTG	GTA	GCT	GGC	TCA	TCC	TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG	2056
G	S	R	H	R	A	E	V	A	S	A	L	R	S	F	S	P	L	Q	P	599
GGC	TCC	AGG	CAC	AGG	GCT	GAA	GTC	GCC	TCT	GCC	CTG	CGC	TCC	TTC	TCC	CCG	CTG	CAA	CCC	2116

Fig. 17D

G	Q	A	P	T	G	R	A	H	S	T	M	T	G	S	G	V	D	A	R	619
GGG	CAG	GCG	CCC	ACA	GCG	CGG	GCT	CAC	AGC	ACC	ATG	ACA	GGC	TCT	GGG	GTG	GAT	GCC	AGG	2176
T	A	S	S	G	S	S	V	W	E	G	Q	L	Q	S	L	V	L	S	E	639
ACA	GCC	AGC	TCC	GGG	AGC	AGC	GTG	TGG	GAA	GGA	CAG	CTG	CAG	AGC	CTG	GTG	CTG	TCA	GAA	2236
Y	A	S	T	E	M	S	L	H	A	L	Y	M	H	Q	L	H	K	Q	Q	659
TAT	GCA	TCC	ACA	GAG	ATG	AGC	CTG	CAT	GCC	CTC	TAT	ATG	CAC	CAG	CTC	CAC	AAG	CAG	CAG	2296
A	Q	A	E	P	E	R	H	V	W	H	R	R	E	S	D	E	S	G	E	679
GCC	CAG	GCT	GAA	CCT	GAG	CGG	CAT	GTA	TGG	CAC	CGC	CGG	GAG	AGT	GAT	GAG	AGT	GGA	GAA	2356
S	A	P	D	E	G	G	E	G	A	R	A	P	Q	S	I	P	R	S	A	699
AGC	GCC	CCT	GAT	GAA	GGG	GGA	GAG	GAG	GCC	CGG	GCC	CCC	CAG	TCT	ATC	CCT	CGC	TCT	GCT	2416
S	Y	P	C	A	A	P	R	P	G	A	P	E	T	T	A	L	H	G	G	719
AGC	TAT	CCC	TGT	GCA	GCA	CCC	CGG	CCT	GGA	GCT	CCT	GAG	ACC	ACC	GCC	CTG	CAT	GGG	GGC	2476
F	Q	R	R	Y	G	G	I	T	D	P	G	T	V	P	R	V	P	S	H	739
TTC	CAG	AGG	CGC	TAC	GGT	GGC	ATC	ACA	GAT	CCT	GGC	ACA	GTG	CCC	AGG	GTT	CCC	TCT	CAT	2536
F	S	R	L	P	L	G	G	W	A	E	D	G	Q	S	A	S	R	H	P	759
TTC	TCT	CGG	CTG	CCT	CTT	GGA	GGG	TGG	GCA	GAA	GAT	GGG	CAG	TCG	GCA	TCA	AGG	CAC	CCT	2596

166/361

Fig. 17E

# REFSeq

E	P	V	P	E	E	G	S	E	D	E	L	P	P	Q	V	H	K	V	*	779			
GAG	CCC	GTG	CCC	GAA	GAG	GGC	TCG	GAG	GAT	GAG	CTA	CCC	CCT	CAG	GTG	CAC	AAG	GTA	TAG	2656			
ACA	AGG	CTG	AGC	AGG	TTCT	GTG	CCCC	AGG	ATG	GAG	GCC	ACCG	CTGCC	CATCC	CGTCT	GCCT	GCC	ATGG	GAC	CGG	2735		
CTC	CTCT	GAG	TGTT	CCCT	TGCCCC	CAC	GTGT	GTG	TGTT	TGT	GTCT	GTG	TGCT	GTG	CCCA	AGG	AGT	GCC	AAC	ACT	2814		
TTG	CCAC	AGCCCC	CAG	GAG	AGGA	ATT	TGG	GGCC	TAG	GAA	CCG	AGG	GCAC	ACGG	ACTCT	AGC	CTCAT	CCCC	AGG	ACCCCC	2893		
TTG	GCTC	AGAG	TGT	GTCT	AGAA	ACT	GGT	CCCC	AGCC	AGT	ACTG	CCCC	AGT	ACT	TAC	ACCT	TAC	CCCC	TG	CAA	GTC	2972	
CCC	AG	GGG	CTG	CCCC	ATAG	AACT	GTG	TCCC	AGC	AGG	AGAA	CCCT	GTG	CCAA	CTGT	GGAG	TGG	GAG	GTG	GGC	CTG	3051	
CCC	TC	AAC	CCCT	GC	AAC	CTT	CCCT	AG	CCCC	CTCA	ATAG	ATG	AG	CAG	GTCA	GGCC	TTAC	CTC	AC	CCG	CAG	3130	
T	CG	CC	AG	TG	CTG	CAG	CCG	GCT	CAC	CTCT	C	CGCT	CTT	CG	CA	CTC	ACT	G	CG	CTG	CTG	3209	
G	TT	CG	CTT	G	CTC	CG	CTT	T	CG	CTT	T	CG	CTT	T	CG	CTT	T	CG	CTT	T	CG	CTT	3288
A	TTT	TG	AC	ACT	AAAA	AG	AGT	TTT	CT	AAAT	TG	AG	AG	CAG	GAT	G	AAAT	ACT	TTG	CTG	CCCT	3367	
T	GG	CCCC	CAG	GACT	GAG	GTCT	CT	CTG	GG	CCCT	CA	TTG	CTG	CTT	AT	CGT	AC	CCCC	CA	TAC	CTG	3446	
C	GG	GCTG	GAG	GTG	ACCT	TG	GCTG	TAC	CGT	CCC	AG	CAAA	AG	AGCT	CTG	GG	CCG	CA	TCT	CG	CTG	3525	
A	T	GA	AG	GG	CG	ATG	CCCT	CG	CC	AG	GGCT	TTG	GG	CTG	CTG	CA	TG	CTG	GG	ACT	G	3604	
C	ACC	AG	CTG	TG	GTCC	GG	CTT	TG	GG	AG	AGT	GGT	GA	ATT	G	CG	CTG	CC	CA	ACT	CG	3683	
A	C	AG	CTG	ATA	AC	CCCT	T	TA	ATA	AAAA	AGG	AGT	TTG	AC	CA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	3762	
G	CG	CG	CG	C	G	C	G	C	G	C	G	C	G	C	G	C	G	C	G	C	G	3770	

Fig. 17F

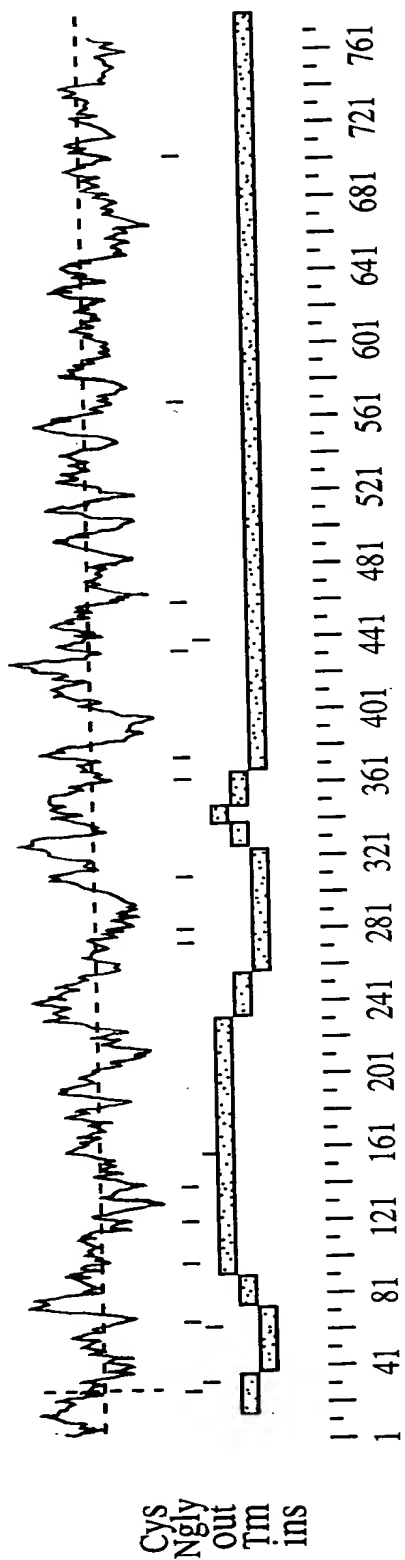


FIG. 176

[illegible]

169/361

G	S	L	I	T	I	L	V	I	A	G	V	F	W	I	H	R	L	I	K	149
GGC	TCC	CTT	ATC	ACC	ATC	CTG	GTC	ATT	GCT	GGT	GTC	TTC	TGG	ATC	CAC	CGG	CTT	ATC	AAG	566
F	I	Y	N	I	C	C	Y	W	E	I	H	S	F	Y	L	H	A	L	R	169
TTC	ATC	TAT	AAC	ATT	TGC	TGC	TAC	TGG	GAG	ATC	CAC	TCC	TTC	TAC	CTG	CAC	GCT	CTG	CGC	626
I	P	M	S	A	L	P	Y	C	T	W	Q	E	V	Q	A	R	I	V	Q	189
ATC	CCT	ATG	TCT	GCC	CTT	CCG	TAT	TGC	ACG	TGG	CAA	GAA	GAG	GTG	CAG	GCC	ATC	GTG	CAG	686
T	Q	K	E	H	Q	I	C	I	H	K	R	E	L	T	E	L	D	I	Y	209
ACG	CAG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	746
H	R	I	L	R	F	Q	N	Y	M	V	A	L	V	N	K	S	L	L	P	229
CAC	CGC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	806
L	R	F	R	L	P	G	L	G	E	A	V	F	F	T	R	G	L	K	Y	249
CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	866
N	F	E	L	I	L	F	W	G	P	G	S	L	F	L	N	E	W	S	L	269
AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	926
K	A	E	Y	K	R	G	G	Q	R	L	E	L	A	Q	R	L	S	N	R	289
AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	986

170/361

Fig. 171

# REF ID: A63460

I L W I G I A N F L L L C P L I L I W Q I	309
ATC CTG TGG ATT GGC ATC GCT AAC TTC CTG CTG TGC CCC CTC ATC CTC ATA TGG CAA ATC	1046
L Y A F F S Y A E V L K R E P G A L G A	329
CTC TAT GCC TTC TGC TAT GCT GAG GTG CTG AAG CGG GAG CCG GGG GCG CTG GGA GCA	1106
R C W S L Y G R C Y L R H F N E L E H E	349
CGC TGC TGG TCA CTC TAT GGC CGC TGC TAC CTC CGC CAC TTC AAC GAG CTG GAG CAC GAG	1166
L Q S R L N R G Y K P A S K Y M N C F L	369
CTG CAG TCC CGC CTC AAC CGT GGC TAC AAG CCC GCC TCC AAG TAC ATG AAT TGC TTC TTG	1226
S P L L T L L A K N G A F F A G S I L A	389
TCA CCT CTT TTG ACA CTG CTG GCC AAG AAT GGA GCC TTC TTC GCT GGC TCC ATC CTG GCT	1286
V L I A L T I Y D E D V L A V E H V L T	409
GTG CTT ATT GCC CTC ACC ATT TAT GAC GAA GAT GTG TTG GCT GTG GAA CAT GTG CTG ACC	1346
T V T L L G V T V T V C R S F I P D Q H	429
ACC GTC ACA CTC CTG GGC GTC ACC GTG ACC GTG TGC AGG TCC TTT ATC CCG GAC CAG CAC	1406
M V F C P E Q L L R V I L A H I H Y M P	449
ATG GTG TTC TGC CCT GAG CAG CTG CTC CGC GTG ATC CTC GCT CAC ATC CAC TAC ATG CCT	1466

171/361

Fig. 17J

D	H	W	Q	G	N	A	H	R	S	Q	T	R	D	E	F	A	Q	L	F	469
GAC	CAC	TGG	CAG	GGT	AAT	GCC	CAC	CGC	TCG	CAG	ACC	CGG	GAC	GAG	TTT	GCC	CAG	CTC	TTC	1526
Q	Y	K	A	V	F	I	L	E	E	L	L	S	P	I	V	T	P	L	I	489
CAG	TAC	AAG	GCA	GTG	TTC	ATT	TTG	GAA	GAG	TTG	CTG	AGC	CCC	ATT	GTC	ACA	CCC	CTC	ATC	1586
L	I	F	C	L	R	P	R	A	L	E	I	I	D	F	F	R	N	F	T	509
CTC	ATC	TTC	TGC	CTG	CGC	CCA	CGG	GCC	CTG	GAG	ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	1646
V	E	V	V	G	V	G	D	T	C	S	F	A	Q	M	D	V	R	Q	H	529
GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	TTT	GCT	CAG	ATG	GAT	GTT	CGC	CAG	CAT	1706
G	H	P	Q	W	L	S	A	G	Q	T	E	A	S	V	Y	Q	Q	A	E	549
GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	GAG	GCC	TCA	GTG	TAC	CAG	CAA	GCT	GAG	1766
D	G	K	T	E	L	S	L	M	H	F	A	I	T	N	P	G	W	Q	P	569
GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	GCC	ATC	ACC	AAC	CCT	GGC	TGG	CAG	CCA	1826
P	R	E	S	T	A	F	L	G	F	L	K	E	Q	V	Q	R	D	G	A	589
CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTC	CTC	AAG	GAG	CAG	GTG	CAG	CGG	GAT	GGA	GCA	1886
A	A	S	L	A	Q	G	G	L	L	P	E	N	A	L	F	T	S	I	Q	609
GCT	GCT	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT	GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	1946

172/361

Fig. 17K



S	L	Q	S	E	S	E	P	L	S	L	I	A	N	V	V	A	G	S	S	629
TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT	ATC	GCA	AAT	GTG	GTA	GCT	GGC	TCA	TCC	2006
C	R	G	P	P	L	P	R	D	L	Q	G	S	R	R	A	H	S	T	M	649
TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG	GGC	TCC	AGG	CGG	GCT	CAC	AGC	ACC	ATG	2066
T	G	S	G	V	D	A	R	T	A	S	S	G	S	S	V	W	E	G	Q	669
ACA	GGC	TCT	GGG	GTG	GAT	GCC	AGG	ACA	GCC	AGC	TCC	GGG	AGC	AGC	GTG	TGG	GAA	GGA	CAG	2126
L	Q	S	L	V	L	S	E	Y	A	S	T	E	M	S	L	H	A	L	Y	689
CTG	CAG	AGC	CTG	GTG	CTG	TCA	GAA	TAT	GCA	TCC	ACA	GAG	ATG	AGC	CTG	CAT	GCC	CTC	TAT	2186
M	H	Q	L	H	K	Q	Q	A	Q	A	E	P	E	R	H	V	W	H	R	709
ATG	CAC	CAG	CTC	CAC	AAG	CAG	CAG	GCC	CAG	GCT	GAA	CCT	GAG	CGG	CAT	GTA	TGG	CAC	CGC	2246
R	E	S	D	E	S	G	E	S	A	P	D	E	G	G	E	G	A	R	A	729
CGG	GAG	AGT	GAT	GAG	AGT	GGA	GAA	AGC	GCC	CCT	GAT	GAA	GGG	GGA	GAG	GGC	GCC	CGG	GCC	2306
P	Q	S	I	P	R	S	A	S	Y	P	C	A	A	P	R	P	G	A	P	749
CCC	CAG	TCT	ATC	CCT	CGC	TCT	GCT	AGC	TAT	CCC	TGT	GCA	GCA	CCC	CGG	CCT	GGA	GCT	CCT	2366
E	T	T	A	L	H	G	G	F	Q	R	R	Y	G	G	I	T	D	P	G	769
GAG	ACC	ACC	GCC	CTG	CAT	GGG	GGC	TTC	CAG	AGG	CGC	TAC	GGT	GGC	ATC	ACA	GAT	CCT	GGC	2426

Fig. 17L



GCTGGAGCGGAGCGCAATGCTCAGCCCTGGATGTAGCTGAGAGGCTGGGAGAAGACGACCGCTGGAGACCG	79
AGCGCGTGCGGAAGACCTAGGGGGTGCGGGAAGCAGACAGGAGAACAACCTCGAAATCAAGCGCTTACAGATTA	158
TTTTTATTTTGTATAGAGAACACGTAGCGACTCCGAAGATCAGCCCCA ATG AAC ATG TCA GTG TTG ACT TTA	8
	229
Q E Y E F E K Q F N E N E A I Q W M Q E	28
CAA GAA TAT GAA TTC GAA AAG CAG TTC AAC GAG AAT GAA GCC ATC CAA TGG ATG CAG GAA	289
N W K K S F L F S A L Y A A F I F G G R	48
AAC TGG AAG AAA TCT TTC CTG TTT TCT GCT TAT GCT GCC TTT ATA TTC GGT GGT CGG	349
H L M N K R A K F E L R K P L V L W S L	68
CAC CTA ATG AAT AAA CGA GCA AAG TTT GAA CTG AGG AAG CCA TTA GTG CTC TGG TCT CTG	409
T L A V F S I F G A L R T G A Y M V Y I	88
ACC CTT GCA GTC TTC AGT ATA TTC GGT GCT CTT CGA ACT GGT GCT TAT ATG GTG TAC ATT	469
L M T K G L K Q S V C D Q G F Y N G P V	108
TTG ATG ACC AAA GGC CTG AAG CAG TCA GTT TGT GAC CAG GGT TTT TAC AAT GGA CCT GTC	529
S K F W A Y A F V L S K A P E L G D T I	128
AGC AAA TTC TGG GCT TAT GCA TTT GTG CTA AGC AAA GCA CCC GAA CTA GGA GAT ACA ATA	589

Fig. 18A

F	I	I	L	R	K	Q	K	L	I	F	L	H	W	Y	H	H	I	T	V	148
TTC	ATT	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAT	CAC	CAC	ATC	ACT	GTG	649
L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	G	W	F	M	T	168
CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTT	GCC	GGG	GGA	GGT	TGG	TTC	ATG	ACT	709
M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	F	188
ATG	AAC	TAT	GGC	GTG	CAC	GCC	GTG	ATG	TAC	TCT	TAC	TAT	GCC	TTG	CGG	GCG	GCA	GGT	TTC	769
R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	M	208
CGA	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	ATG	829
G	C	V	V	N	Y	L	V	F	C	W	M	Q	H	D	Q	C	H	S	H	228
GGC	TGT	GTG	GTT	AAC	TAC	CTG	GTC	TTC	TGC	TGG	ATG	CAG	CAT	GAC	CAG	TGT	CAC	TCT	CAC	889
F	Q	N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	H	248
TTT	CAG	AAC	ATC	TTC	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	CAT	949
F	F	F	E	A	Y	I	G	K	M	R	K	T	T	K	A	E	*			266
TTC	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	ATG	AGG	AAA	ACA	ACG	AAA	GCT	GAA	TAG			1003
TGTTGGA	ACTGAGGAGG	AAGCCATAGCTCAGG	GTCAATAGACAAA	AATATAGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	AAATGACAAA	1082
ACGTGGT	GAGCTAAA	ACAAAACATGAGCA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	AAACACAA	1161

Fig. 18B

CCCAGTAAGTTTATGATCCCTTTTAGGGTGAGGACTCACTGAGTGCACCTCCATCTCCAAGCACTGCTGCTGGAAGACCC 1240  
 CATTCCTCTTTATCTATCAACTCTAGGACAAAGGGAGAACAAAGCAAGCCAGAACGAGAGAGACTAATCAAGGCAA 1319  
 ACAAGGCTATTAAACACATAGGAAAAAATGTAATTTACTAAGTGTACATTTCTCTAAGATGAAAAGATTTTACTCTAGA 1398  
 AACTGTGCGAGCCAAACACACACAATCCTTTCTAACTTTATGGACACTAAACTGGAGCCAAATAGAAAAAGACAAAAATGA 1477  
 AAGAGACACAGGGTGTATATCTAGAACGATAATGCTTTTGGCAGAAACTAAAGCCTTTTAAAGAAATGCCAGCTGCTGTA 1556  
 GACCCCATGAGAAAAAGATGTCCTTAATCATCCTTATGAAAAACAGATGTAAACAACATAATTTCAACTAACTTCATCTTCA 1635  
 CTGCATAGCCTCAGGCTAGTGAGTTTGCCAAAACCAAGGGGTGAATACTTCCCCAAGATTCTTCTGGGAGGATGGA 1714  
 AACAGTGCAGCCCGAGTCCCATGGGGCAGCTCCATCCAGAGCATTTCTGATAGTTGAACTGTAATTTCTACTCTTAA 1793  
 GTGAGATATGAAGCATTATCCTTTTGTTCAGTTGCCCCGGCTTTTGAAACAGAAAGAGTAAATACAGAAATTGAAAAAGAT 1872  
 AAACACTCAACCAACAATGTGAAAAACGGGTTCTGTAGTATTTGTAAAAAGGCCCGCCAGGACCACTGTGAGCTGGA 1951  
 AAAGGGAGAAAGGCAGTGGGAAAAGAGGTGAGCCGAAGATCAATTCGACAGACAGACGGTGTGTATGCCCTCCCTGTT 2030  
 TGACTTCACACACACTCATAACTTTCCAAATGAAACCCACAGTATAGCGCATATTTTCGATATTTTGTGAAATTCCAA 2109  
 AAGGAAATCACAGGGCTGTTGAAAATATTGGGGGAAACACTGTGTTTCTGCATCATCTGCATTTGCTCCCCAAGCAAATGT 2188  
 AGAGGTGTTTAAAGGGCCCTCTGCTGGCTGAGTGGCAATACTACAACAACTTCAAGGCAAGTTTGGCTGAAAAACAGTT 2267  
 GACAACAAAAGGGCCCCCATACACTTATCCCTCAAATTTTAAAGTGATATGAAATACCTTGTCAATGCTTTGGCCAAATCAG 2346  
 AAGATATTCACTCCTGCTTCAAGTCAGCTTCAGAAATGTTTAAAGGGACTTTAGCTCTGGAACCTCAAAATCAATTTAT 2425  
 TAAGAGCCATATTTCTTAAAAAAAAGCTGGATAAATATTTCTGTGTAATATTTTCAGTCCCTTTACAAGCCAAAATACATG 2504  
 TGTCAAATGTTTCTAGTATTTCAAAGAAGCAATTATGTAAAGTTGTTCAATGTGACATAAATAGTATTTATAATTGGTTAAG 2583  
 TAGCTTAATGATTAGGCAAACTAGATGAAAAGATTAGGGGCTTCCACACTGCATAGATTACACGCACATAGCCACGCAT 2662  
 ACACACACAGACACACAGATGTGGGGTACACTGAACTTCAAAGCCCCAAATGAATAGAAAACACATTTTCTGGCTAGCAGA 2741  
 AAAAAACAAAAAACAACCTGTTGTTTCTCTTTCTTGTGAGAGGTACAGTAAAAGGGATTTTTCGAATTATTTTA 2820  
 TATTATTTTAGCTTTAATTGTGCTGCTGCTCATGAAACAGAGCTGCTCTGCTTTTCTGTCTAGAGATGGCAAGGCTTTT 2899  
 TCAGCATCTCGTTTATGTGTGGAATTTAAAAAGAAATAAAGTTTATTTCCATTTCTGTGTGAAAAAAAATAAAAAAAA 2978  
 AAAAAA

Fig. 18C

L	K	Q	S	V	C	D	Q	S	F	Y	N	G	P	V	S	K	F	W	19	
GC	CTG	AAG	CAG	TCA	GTT	TGT	GAC	CAG	AGT	TTT	TAC	AAT	GGA	CCT	GTC	AGC	AAA	TTC	TGG	59
A	Y	A	F	V	L	S	K	A	P	E	L	G	D	T	I	F	I	I	L	39
GCT	TAT	GCA	TTT	GTG	CTC	AGC	AAA	GCA	CCC	GAA	CTA	GGT	GAC	ACG	ATA	TTC	ATC	ATT	CTG	119
R	K	Q	K	L	I	F	L	H	W	Y	H	H	I	T	V	L	L	Y	S	59
AGG	AAA	CAG	AAA	CTG	ATC	TTC	CTG	CAC	TGG	TAC	CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCC	179
W	Y	S	Y	K	D	M	V	A	G	G	G	W	F	M	T	M	N	Y	G	79
TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTC	GCT	GGG	GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC		239
V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	F	R	V	S	R	99
GTG	CAT	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	CGG	GCT	GCG	GGT	TTC	CGA	GTC	TCC	CGG	299
K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	M	G	C	V	I	119
AAG	TTT	GCC	ATG	TTC	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	359
N	Y	L	V	F	N	W	M	Q	H	D	N	D	Q	C	Y	S	H	F	Q	139
AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	AAC	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	419
N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	H	F	F	159
AAC	ATC	TTC	TGG	TCC	TCG	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	CAT	TTC	TTC	479

Fig. 18E



F	E	A	Y	I	G	K	K	V	K	K	A	T	K	A	E	*	175
TTT	GAG	GCC	TAC	ATC	GGC	AAA	GTG	AAG	AAA	GCC	ACG	AAG	GCT	GAG	TAG		527
TGTCAGGGCTGAGGAGGAAGTCATAGCTCAGGGTCATCAGGAAAAATAATCGACAAAAAAGAAAAATGGCACAAAGGAATCC	606																
CATATGGTGCAGCTAAAAACAACAAACATCCGTATGAGCAGGCACGAGGCCAAAGCAGCTTGGGACTGAAGATTAG	685																
GTTGTAAGTTTATGATCCTTCTGGGTGAGGACTCGCTGAGTGCAACTCTTATCTCAAAGCACGGCTGCTGAGGGGACC	764																
CCTTCCCTCTGGCCTGTCAACTCTAGAACACACTAGATGCAAAGGCAGCCACGGGCAAAGAGATTGGGCAGAGATTAGT	843																
GGACGGCCAGCAAAACACTGCAGGAAGCAGGTGGGGGAGGAATCTACTCAGCCCTTTTGTGTTTGTGTTTGTGTTT	922																
GTTTTTCTCTAAGGATAAAGGAGTTTCCCTTTTCAAACGATGTGAGCACACACACACACACACACACACACACA	1001																
CACACACACACACGCAATCTTTTCAACACGAAACCCAGAGCTAAAAAGAAAAGATAAACATGGGAGAGACAGGGTTTCTAT	1080																
CTGGGACAGCAATGCTTTTGCAAAAGGCTAGGCCCTTTTAAAGAAAAGGTGAGCTTGTAACCTCCTTGATAAAAAGATGCTT	1159																
AATTATTTTACTGCAACTGAAAGTAAAGAGGTAGAGCCCTTTCCCTTCTGCACAGCCTCAGGGCTTGTAATGTTCTCTA	1238																
CAACCAACACACAGGACAGTACTTCCCCCATGATACTTTATTACTGGGAGAAAAGAAACCCCTGTAGTTGAAACACCCACAC	1317																
TGACAACTGTTATTCTGCTCTCCGACGAGAAATCAAGCATCCGTTGTTTCAGTTGCCCCCAAACCTTTAGGACGGAGGAGT	1396																
AAATGCAGAACTGAAAAGGGAAGACTCAGCTGGCTGGCTTGAAAATGGAGTCTTGTAACCATGTGTAACAAATGCCAGC	1475																
CCATCGTCCCTGGAGCTGAACAGGGAGGAAGGCTATGGCAGAGACTAGAGCCGGATTCAATCCAAATGTGCAGACAGCG	1554																
TGTTGCGCTCCCTGTTTCGACCTCACACATAATCCTGGCTTCTAAATGAGGCCCTGTGACACACTCTGTGCTTTC	1633																
TATATTTTGTGACTTTCAAACACAGATCTGCAGGGCTCTGCCCTGATTTGGGGTAAACACTGTGTTTCTGCAGCCTCTG	1712																
CATTGCTCCCTTCAGCAGTGCAGAGGCTTGAGAAAGTGCCCTCTGCTGGCTTAGTGAGAAGCTTCAACAAACACTTCAC	1791																
AGTAGGTTGAAATAACTGACCACCTAAGGGCCTGCGGAGATTAAACCCCTAAGTTCTAAGTGTCTCAACACACCTGACATA	1870																
TATTTGACCAAAATCAGAAGAGAGAGAGAACCTCTATGCTTCAAGTAAGCGTCATAAATTTTTTAAGTGACTTTCACCTG	1949																
AGAACTCAGAAAGTCAATGTATTAAAGAGCCATATTCTGAAAGAAAAGAGAAAAGAAAAGAAAAA	2028																
AAAA	2032																

Fig. 18F



102110-0215260

181/361

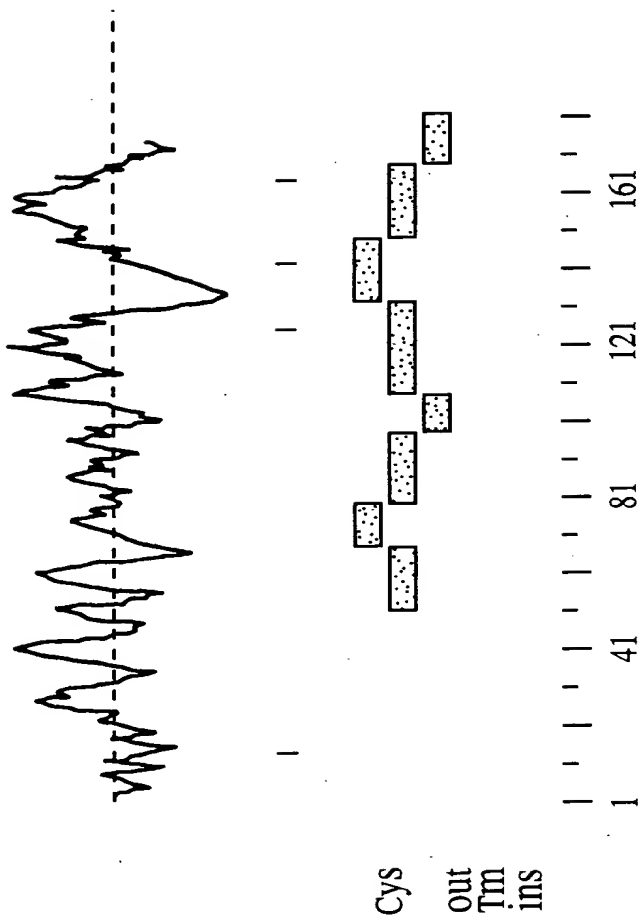


FIG. 186



**Fig. 18I**

human	290	300	310	320	330	340	350
	TGAAGCAGTCAGTTTGTGACACAGGGTTTTTACAATGGACCTGT	CAGCAAATCTGGGCTTATGCATTGT					
murine	10	20	30	40	50	60	70
	TGAAGCAGTCAGTTTGTGACACAGAGTTTTTACAATGGACCTGT	CAGCAAATCTGGGCTTATGCATTGT					
human	360	370	380	390	400	410	420
	GCTAAGCAAAGCACCCGAACTAGGAGATACAATATTCATTATTCT	GAGGAAGCAGAAGCTGATCTTCCTG					
murine	80	90	100	110	120	130	140
	GCTCAGCAAAGCACCCGAACTAGGTGACACGATATTCATTCATTCT	GAGGAAACAGAAAACCTGATCTTCCTG					
human	430	440	450	460	470	480	490
	CAC TGGTATCACCCACATCACTGTGCTCCTGTACTCTTGGTACTCCT	ACAAAGACATGGTTGCCGGGGGAG					
murine	150	160	170	180	190	200	210
	CAC TGGTACCACCCACATCACTGTGCTCCTGTACTCCTGGTACTCCT	ACAAAGACATGGTCGCTGGGGTG					
human	500	510	520	530	540	550	560
	GTTGGTTCATGACTATGAAC TATGGCGTGCACGCCG TGATG TACTCTTACTATGCCTT	GCGGGCGGCAGG					
murine	220	230	240	250	260	270	280
	GTTGGTTCATGACTATGAAC TATGGCGTGCATGCCGTCA TG TACTCTTACTACGCCTT	GCGGCTGCCGGG					

184/361

**Fig. 18K**



ref00065460

```

10      20      30      40      50      60
I400 ATGAACATGTCAGTGTGACTTTACAAGAATATGAATT--CGAAAAGCAGTTCAACGAGAATGAAGC--
      :::::  ::  ::::  ::  :::::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
CIG30 ATGGACACATCCATGAATTTCTCACGCGGGTTAAAAAATGGACCTGATGCAACCCCTATGACTTCGAGACGT
      10      20      30      40      50      60      70

      70
I400 --CA--TCCAATGG-----ATGCAGGAAAACCTGGAAGAAATCTTTCCT-GTTTTCTGC-TCTGTATGCT
      ::  ::  ::::  ::  :::::  ::  ::::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
CIG30 TTCAGGACTTAAGGCCCTTTTGGAGGAGTACTGGGTAAGCTCATTTCTCATAGTGTGTCGTCTATCTGTT
      80      90      100     110     120     130     140

      130     140     150     160     170     180     190
I400 GCCTTTATATTCGGTGGTCGGCACCTA-ATGAATAAACGAGCAAAAGTTTGAAC-T-GAGGAAGCCATTAGT
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
CIG30 GC--TCATCGTTGTTGGCCAG-ACCTACATGAGAACGCGGA-AGAGCTTCAGCTTGCAGAGGCCCTCTCAT
      150     160     170     180     190     200

      200     210     220     230     240     250     260
I400 GCTCTGGTCTCTGACCCCTTGACGTCTTCAGTATATTCGGTGCTCTTCGAACTGGTGCTTATATGGGTGAC
      :::::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
CIG30 CCTCTGGTCCTTCTTCCCTGGCAATATTCAGTATCCTCTGGGTACTCTGAGGATGTGGAAGTTTATGGCAACA
      210     220     230     240     250     260     270

```

**Fig. 18M**

[illegible]

188/361



**Fig. 180**

# Sequence

L	G	D	T	I	F	I	I	L	R	K	Q	K	L	I	F	L	H	W	Y	20
CTA	GGT	GAT	ACG	ATA	TTC	ATC	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAC	60
H	H	I	T	V	L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	40
CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTA	GCT	GGG	GGT	120
G	W	F	M	T	M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	60
GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	GTA	CAC	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	180
R	A	A	G	F	R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	80
CGG	GCT	GCG	GGT	TTC	CGG	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACG	TTG	TCC	CAG	ATC	240
T	Q	M	L	M	G	C	V	I	N	Y	L	V	F	N	W	M	Q	H	D	100
ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	300
N	D	Q	C	Y	S	H	F	Q	N	I	F	W	S	S	L	M	Y	L	S	120
AAT	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	AAC	ATC	TTT	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	360
Y	L	L	L	F	C	H	F	F	F	E	A	Y	I	G	K	V	K	K	A	140
TAC	CTT	CTG	CTC	TTC	TGC	CAT	TTC	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	GTG	AAG	AAA	GCG	420
T	K	A	E	*																145
ACG	AAG	GCC	GAG	TAG																435

190/361

Fig. 18P

TGT CAGAGCTGAGGAGGAAAGACATAGCTCAGGGTCATCACGAAAAATAATAGACAAAAAAGAAAAATGGCACAAAGGAATCA 514  
 CATATGGTGCAGCTAAACAACAAAAACATATAGCAGACGCTAAGCCCAAGCAGCTTGGGAGTGAAGATTAGGTT 593  
 GTAAGTTTATGATCCCTTTTGGGTGAGGACTCACTGAGAACACTGCTGCTGAGGACCCCTTCCCTCTTACCTGTCAA 672  
 CTCTAGAACACACTAGAAGCCAAAGCAGCCATGGGCAAGGAGATTAGTGGACAGCAAGCAAAACACTGCAGGAAGAGGG 751  
 GGGAGATCTATTTCAGAGTTTTTTGTTTTGTTTTGTTCTCTAAGGATAAAGGAGTTTCCCCCTTTTCAAACTG 830  
 TGTGAGCACACCCACCGGCATGCAGACACACCCACCTACACACTATCTGCAGATGACCAGTGTCCCTATGCTGTTTTTAC 909  
 AAATAAACTTGAGACAAGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 974

**Fig. 18Q**

Fig. 18R

	10	20	30	40	50	60	70		
human	MNMSVLT	QEQFNEN	EAIQWMQ	ENWKSFL	FSALYAA	FI FGGRHLM	KNKRAK	FELRKPLVLSLTL	
murine	-----	-----	-----	-----	-----	-----	-----	-----	
rat	-----	-----	-----	-----	-----	-----	-----	-----	
human	AVFSIFG	ALRTGAY	MVYIILM	TKGLKQ	SVCDQGF	YNGPVS	KFWAYAF	VLSKAPELGD	TIFILRKQKLIFL
murine	-----	-----	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----	-----	-----
human	HWYHHIT	VLLYSW	YSYKDM	VAGGGWF	MTMNYG	VHAVMYS	YALRAA	GFRVSRKFAM	FITLSQITQMLMGC
murine	HWYHHIT	VLLYSW	YSYKDM	VAGGGWF	MTMNYG	VHAVMYS	YALRAA	GFRVSRKFAM	FITLSQITQMLMGC
rat	HWYHHIT	VLLYSW	YSYKDM	VAGGGWF	MTMNYG	VHAVMYS	YALRAA	GFRVSRKFAM	FITLSQITQMLMGC
human	VVNYLV	FCWMQ	HD - -	QCHSHF	QNI FWSS	LMYLSY	LVLFCH	FFFEAYI	GKMRKTTKAE
murine	VINYLV	FNWMQ	HDNDQ	CYSHFQ	NI FWSS	LMYLSY	LVLFCH	FFFEAYI	GKVKKATKAE
rat	VINYLV	FNWMQ	HDNDQ	CYSHFQ	NI FWSS	LMYLSY	LVLFCH	FFFEAYI	GKVKKATKAE

Fig. 18R

# Sequence

GTCGACCCACGCGTCCGGGAGCGCGGCTAAGAGTGCCCGCACCGCCTCACAAACCTGGGAACCGGAGAGTAGGGCCGTC	79
GGCTGGCAAGAACC CGCGTGCCTCCTCGGCAAGGGCCATCCGGTGCCACCCATGTGCGCACTAGAGCAGAGAGGGTGA	158
<div style="text-align: center;">M T W L V</div>	
GTCCTGAACCTGCAACCTGCACAGAGCTGCTCTGTACTGTCCCTGGTGGTCCCGCC ATG ACC TGG TTG GTG	229
L L G T L L C M L R V G L G T P D S E G	25
CTG CTG GGG ACA CTG CTC TGC ATG CTG CGC GTT GGG TTA GGC ACC CCG GAC TCC GAG GGT	289
F P P R A L H N C P Y K C I C A A D L L	45
TTC CCG CCC CGT GCG CTC CAC AAC TGC CCC TAC AAA TGT ATC TGC GCT GCC GAC CTG CTA	349
S C T G L G L Q D V P A E L P A A T A D	65
AGC TGC ACT GGC CTA GGG CTG CAG GAC GTG CCA GCC GAG TTA CCT GCC GCT ACT GCG GAC	409
L D L S H N A L Q R L R P G W L A P L F	85
CTC GAC CTG AGC CAC AAC GCG CTC CAG CGC CTG CGC CCC GGC TGG TTG GCG CCC CTC TTC	469
Q L R A L H L D H N E L D A L G R G V F	105
CAG CTG CGC GCC CTG CAC CTA GAC CAC AAC GAA CTA GAT GCG CTG GGT CGC GGC GTC TTC	529
V N A S G L R L L D L S S N T L R A L G	125
GTC AAC GCC AGC GGC CTG AGG CTG CTC GAT CTA TCA TCT AAC ACG TTG CCG GCG CTT GGC	589

193/361

Fig. 19A

# Figure 19B

R	H	D	L	D	L	G	L	G	A	L	E	K	L	L	L	F	N	N	R	L	145
CGC	CAC	GAC	CTC	GAC	GGG	CTG	GGG	CTG	GCG	CTG	GAG	AAG	CTG	CTT	CTG	TTC	AAT	AAC	CGC	TTG	649
V	H	L	D	E	H	A	F	H	G	L	R	A	L	S	H	L	Y	L	G	165	
GTG	CAC	TTG	GAC	GAG	CAT	GCC	TTC	CAC	GGC	CTG	CGC	GCG	CTC	AGC	CAT	CTC	TAC	CTG	GGC	709	
C	N	E	L	A	S	F	S	F	D	H	L	H	G	L	S	A	T	H	L	185	
TGC	AAC	GAA	CTC	GCC	TGC	TTC	TCC	TTC	GAC	CAC	CTG	CAC	GGT	CTG	AGC	GCC	ACC	CAC	CTG	769	
L	T	L	D	L	S	S	N	R	L	G	H	I	S	V	P	E	L	A	A	205	
CTT	ACT	CTG	GAC	CTC	TCC	TCC	AAC	CGG	CTG	GGA	CAC	ATC	TCC	GTA	CCT	GAG	CTG	GCC	GCG	829	
L	P	A	F	L	K	N	G	L	Y	L	H	N	N	P	L	P	C	D	C	225	
CTG	CCG	GCC	TTC	CTC	AAG	AAC	GGC	CTC	TAC	TTG	CAC	AAC	AAC	CCT	TTG	CCT	TGC	GAC	TGC	889	
R	L	Y	H	L	L	Q	R	W	H	Q	R	G	L	S	A	V	R	D	F	245	
CGC	CTC	TAC	CAC	CTG	CTA	CAG	CGC	TGG	CAC	CAG	CGG	GGC	CTG	AGC	GCC	GTG	CGC	GAC	TTT	949	
A	R	E	Y	V	C	L	A	F	K	V	P	A	S	R	V	R	F	F	Q	265	
GCG	CGC	GAG	TAC	GTA	TGC	TTG	GCC	TTC	AAG	GTA	CCC	GCG	TCC	CGC	GTG	CGC	TTC	TTC	CAG	1009	
H	S	R	V	F	E	N	C	S	S	A	P	A	L	G	L	K	R	P	E	285	
CAC	AGC	CGC	GTC	TTT	GAG	AAC	TGC	TGC	CCA	GCT	CTT	GGC	CTA	AAG	CCG	CCG	GAA	GAA	1069		

Fig. 19B

E H L Y A L V G R S L R L Y C N T S V P 305  
 GAG CAC CTG TAC GCG CTG GTG GTG GGT CGG TCC CTG AGG CTT TAC TGC AAC ACC AGC GTC CCG 1129  
  
 A M R I A W V S P Q Q E L L R A P G S R 325  
 GCC ATG CGC ATT GCC TGG GTT TCG CCG CAG CAG GAG CTT CTC AGG GCG CCA GGA TCC CGC 1189  
  
 D G S I A V L A D G S L A I G N V Q E Q 345  
 GAT GGC AGC ATC GCG GTG CTG GGC GAC GGC AGC TTG GCC ATA GGC AAC GTA CAG GAG CAG 1249  
  
 H A G L F V C L A T G P R L H H N Q T H 365  
 CAT GCG GGA CTC TTC GTG TGC CTG GGC ACT GGG CCC CGC CTG CAC CAC AAC CAG AGC CAC 1309  
  
 E Y N V S V H F P R P E P E A F N T G F 385  
 GAG TAC AAC GTG AGC GTG CAC TTT CCG CGC CCA GAG CCC GAG GCT TTC AAC ACA GGC TTC 1369  
  
 T T L L G C A V G L V L V L L Y L F A P 405  
 ACC ACA CTG CTG GGC TGT GCC GTG GGC CTT GTG CTC GTG CTG CTC TAC CTG TTC GCC CCA 1429  
  
 P C R C C R A C P L P L P L A P N T Q P 425  
 CCC TGC CGC TGC TGC CGT GCC TGC CGG TGC CCG CTG CCG CCG CTG GCC CCA AAC ACC CAG CCC 1489  
  
 A P R A E P H K S S V L S T T P P D A P 445  
 GCT CCA AGA GCT GAG CCG CAC AAG TCC TCA GTA CTC AGC ACC ACA CCG CCA GAC GCA CCC 1549

195/361

Fig. 19C

# Sequence

S	P	Q	G	Q	A	S	T	S	T	*		
AGC	CCG	CAA	GGC	CAA	GCG	TCC	ACA	AGC	ACG	TAG	456	
											1582	
TCT	TCT	GAG	CCAG	CCGAG	GGCCCT	CAAT	GGCCCG	CGTG	CAGCT	GGCAGTAGCT	GAGGAAT	TCGATCTCTACAACC 1661
CTG	GAG	CCCTG	CAGCT	GAGGCT	GGCTCT	GAGTCC	GCAGCT	CCATAG	GCTCCG	AGGTCCCATG	ACAACCTAGACTGC 1740	
CAG	GGCT	CCCC	ACCC	CCCC	ACCCCT	CTTGCT	GTCTG	CGCCCT	GTCTCC	CTGCTCCAGAGAACT	GGCAGATACT 1819	
GGT	GGAA	GCACT	GTGC	CTGG	CCCCCAG	CTTCCT	GTATG	GGCCTC	GAAACACA	ATGGGCCCTTCTCGCTCACTGGTAGA 1898		
GAC	AGGG	TTGT	GGT	CCCC	AACCTG	CCCTTCT	GTCTG	CCCCCT	GCACAG	GACCCCAAAGGCCCTGCAAGGTGTG 1977		
CTAG	TTCC	TGCT	TTCC	CGCG	GACTTC	CTAGT	GCCCCAA	ATGCCC	CTGTG	AGGCTGAGAGACCCAGGCCCTGTGGCTTTCA 2056		
ACAC	AGCAC	AGCTGT	GGAA	GTGG	CTGTGT	TCTTCT	TACAG	CCCTGT	GGAAGA	ACCCCTGTAGCAGAGCCCTCCCATCCACCC 2135		
TCAG	GGGCT	GAGGC	AGCTCT	CGAG	GAGTGGT	GTGCTCA	AGAGCT	GACGC	AGGGCC	ACCTCCCCCTTCCCAAGGGGTGGGAG 2214		
GGAG	TGGG	CCCA	CAGGG	AAAAG	AGGGG	CTCTGA	AGGA	AGATCT	CGCCCC	CACACCCCGAGACAGAAAGGAAACAAGC 2293		
CCG	CCCT	CTGG	TGAA	ATGG	GACTCC	CTCCAT	CCACCA	CAACCC	CAACCT	CTGAAAGCTTCACAACTTCACGCAGAGTCC 2372		
GGT	GGC	AGCAC	AGG	CAAG	GGCTCCT	CAAG	AGGTTCC	TGGT	CTGG	CCTAAGCCCCAGCCAGAGGCCCTGCTC 2451		

Fig. 19D



TCTCTGGCCCTGGGGCATCCACCCGTTGTTCTGAAGGCAGAGCCCATTTCTGTGGGCTCACAAAGACACAGTGAAGGGGATC 2530  
 ATGGCCCTGCACCCCTGCTTTTCAGCAGTAAAAAGCCCCGAAAGCCCTGGCGAGCATGGCCGAGCTGGGAGGGCCCGAGCCG 2609  
 GAACTCCACGTCCCTCGAGAGCAGGAGCCCTCTTAAGGGCTGGCACTGGTCTCAGCCCTAATGGCTGAGGCGGTACCCCTGG 2688  
 CTTCATATGCATCTCACTGCTCCCACTGCAGGGGGGCAGGGAAGGGGGTCTGGGAGCCCTTTCATGTGTGGGGGCCGAG 2767  
 CTGGGGCCCCCATGGCCATCCTGGACCTCGCTGCTCCAGAGTTTAATAAAGGTAGCACATGCTTATTGCTAGAAAAAA 2846  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2895

**Fig. 19E**

FIG. 19F

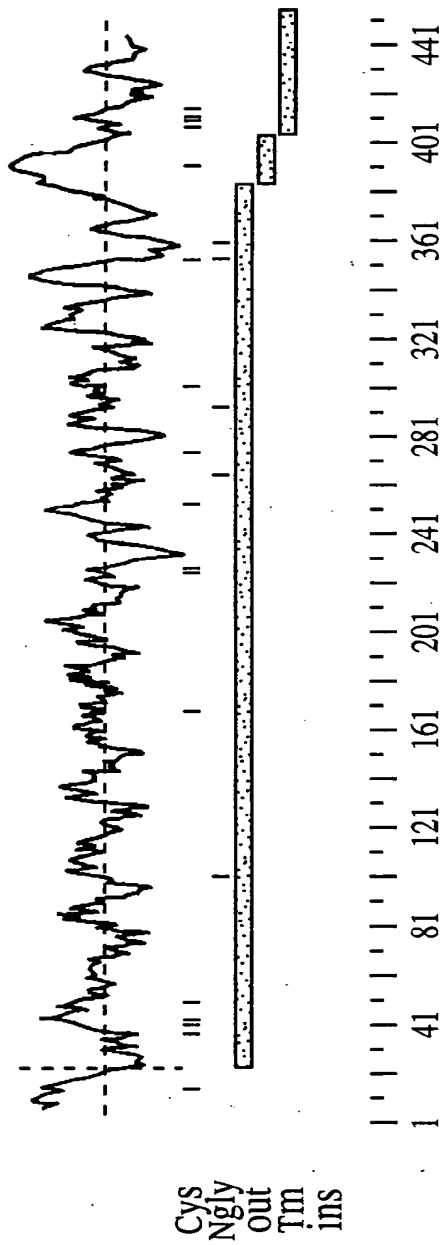


FIG. 19F

10	20	30	40	50	60	70
H	MTWLVLGTLMLRVGLGTPDSEGFPPRALHNCYPKICAADLLSCTGLGLQDVPAELPAATADLDSH					
:	:	:	:	:	:	:
:	:	:	:	:	:	:
P	MN-LDIHCEQLSDARWTELLPLLQQYEVVRLLDDCGLTEEHCKDIGS--ALRANPSLTELCLRTNEL--GD					
10	20	30	40	50	60	
80	90	100	110	120	130	
H	NALQRLRPGWLAPLFQLRALHLDHNELDALGRGVFVNA---SGLRLDLLSSNTLRALGRHDL-DGLGA-					
:	:	:	:	:	:	:
:	:	:	:	:	:	:
P	AGVHLVLQGLQSPCTCKIQKLSLQNCSLTEAGCGVLPSTLRSLPTLRELHLSNDNPLGDAGLRLLCEGLLDP					
70	80	90	100	110	120	130
140	150	160	170	180	190	200
H	---LEKLLLFNNRLVHLD-EHAFHGLRALSHLYLGCNELASFDFDHLHGLSATHLLTDLSSNRLGHISV					
:	:	:	:	:	:	:
:	:	:	:	:	:	:
P	QCHLEKLQLEYCRLLTAASCEPLASVLRATRAL----KELTVSNND--IGEAGARVLGQGLAD-----SA					
140	150	160	170	180	190	
210	220	230	240	250	260	
H	PELAALPAFLKN-GLYLHNNPLPCDCRLYHLLQRWHQRLSAVRDFAREYVCLAFKVPASVR---FFQH					
:	:	:	:	:	:	:
:	:	:	:	:	:	:
P	CQLETLR--LENCGLTPANCKDLGCGIVASQASLRELDLGSNGGLGDAGIAELCPGLLSPASRLKTLWLWEC					
200	210	220	230	240	250	260

Fig. 19G

```

270      280      290      300      310      320
H SRVFENCSSA-PALGLKRPEEHLVALVGRSL-----RLYCNTSV-PAMRIAWVSPQQELLRAPGSRDGS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
P DITASGCRDLCRVLQAKETLKL-SLAGNKLGDGARGLLCESLLQPGCQLESILWVKSCSLTAACQHVSL
270      280      290      300      310      320      330

330      340      350      360      370      380      390
H AVLADGSLAIGNVQEQHAGLFVCLATGPRRLHHNQTHEYNVSVHFPRPEPEAFNTGFTLLGCAVGLVLVL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
P MLTONKHL-----LELQSSNKLGDSGIQELCQALSOPGTTLRVLCIGDCEVTNSGCCSSLAS--LLLANRS
340      350      360      370      380      390

400      410      420      430      440      450
H LYLFAPPCRRACPLPPLAPNTQPAPRAEPHK-SSVLSTTPPDAPSPQGQASTS-----T
: . . . : : : : : : : : : : : : : : : : : : : : : : : :
P LRELDLSNNCVGDPGVLLQSLGSLQPGCALEQLVLYDTYWTEEVEDRLQALEGSKPGLRVIS
400      410      420      430      440      450

```

Fig. 19H

# Sequence

ccg ttt ctc ttt aac cac ttg cac ggt ctg ggg tta acc cgc ctg cgg 48  
 Pro Phe Leu Phe Asn 5 His Leu His Gly Leu Thr Arg Leu Arg 15  
 1  
 act ctg gac ctc tcc tcc aac tgg ctg aaa cat atc tcc atc cct gag 96  
 Thr Leu Asp 20 Leu Ser Ser Asn Trp 25 Lys His Ile Ser 30 Pro Glu  
 ttg gct gca ctg cca act tat ctc aag aac agg ctc tac ctg cac aac 144  
 Leu Ala Ala Leu 35 Tyr Leu 40 Tyr Arg Leu 45 His Asn  
 aac ccg ctg ccc tgt gac tgc agc ctc tac cac ctg ctc cgg cgc tgg 192  
 Asn Pro Leu Pro Cys Asp 55 Cys Ser Leu Tyr His Leu 60 Arg Arg Trp  
 50  
 cac cag cgg ggc ctg agt gcc ctg cat gat ttt gaa cgc gag tac aca 240  
 His Gln Arg Gly Leu Ser 70 Ala Leu His Asp Phe Glu Arg Glu Tyr Thr 80  
 65  
 tgc ttg gtc ttt aag gtg tca gag tcc cga gtg cgc ttt ttt gag cac 288  
 Cys Leu Val Phe 85 Lys Val Ser Glu Ser Arg Val Arg Phe Phe Glu His 95  
 90  
 agc cgg gtc ttc aag aac tgc tct gtg gct gca gct cca ggc tta gag 336  
 Ser Arg Val Phe 100 Lys Asn Cys Ser Val Ala Ala Pro Gly Leu Glu 110  
 105

Fig. 19I

# Sequence

ctg cct gaa gag gag cag ctg cac gcg cag gtg ggc cag tcc ctg agg ctc	384
Leu Pro Glu Glu Gln Leu His Ala Gln Val Gly Gln Ser Leu Arg Leu	
115 120 125	
ttc tgc aac acc agt gtg cct gcc act cgg gtg gcc tgg gtc tcc ccg	432
Phe Cys Asn Thr Ser Val Pro Ala Thr Arg Val Ala Trp Val Ser Pro	
130 135 140	
aag aat gag ctg ctt gtg gcg cca gcc tct cag gat ggt agc atc gct	480
Lys Asn Glu Leu Leu Val Ala Pro Ala Ser Gln Asp Gly Ser Ile Ala	
145 150 155 160	
gtg ttg gct gat ggc agc tta gcc ata ggc agg gtg caa gag cag cac	528
Val Leu Ala Asp Gly Ser Leu Ala Ile Gly Arg Val Gln Glu Gln His	
165 170 175	
gca ggc gtc ttt gtg tgc ctg gcc agt ggg ccc cgc ctg cac cac aac	576
Ala Gly Val Phe Val Cys Leu Ala Ser Gly Pro Arg Leu His His Asn	
180 185 190	
cag aca ctt gag tac aat gtg agt gtg cca aag gct cgc ccc gag cca	624
Gln Thr Leu Glu Tyr Asn Val Ser Val Gln Lys Ala Arg Pro Glu Pro	
195 200 205	
gag act ttc aac aca ggc ttt acc acc ctg ctg ggc tgt att gtg ggc	672
Glu Thr Phe Asn Thr Gly Phe Thr Thr Leu Leu Gly Cys Ile Val Gly	
210 215 220	

**Fig. 19J**

# Figure 19K

ctg gtg ctg gtg ttg ctg tac ttg ttt gca cca ccc tgt cgt ggc tgc Leu Val Leu Val Leu Leu Tyr Leu Phe Ala Pro Pro Cys Arg Gly Cys 225 230 235 240	720
tgt cac tgc tgc cag cgg gcc ggc tgc cgc aac cgt tgc tgg ccc cgg gca Cys His Cys Cys Gln Arg Ala Cys Arg Asn Arg Cys Trp Pro Arg Ala 245 250 255	768
tcc agt cca ctc cag gag ctg agc gca cag tcc tcc atg ctt agc act Ser Ser Pro Leu Gln Glu Leu Ser Ala Gln Ser Ser Met Leu Ser Thr 260 265	816
acg cca cca gat gca ccc agc cgc aag gcc agt gtc cac aag cat gtg Thr Pro Pro Asp Ala Pro Ser Arg Lys Ala Ser Val His Lys His Val 275 280 285	864
gtc ttc ctg gag ccg ggc gag aag aag ggc ctc aat ggc cgt gtg cag ctc Val Phe Leu Glu Pro Gly Lys Lys Gly Leu Asn Asn Gly Arg Val Gln Leu 290 295 300	912
gca gta cct cca gac tcc gat ctg tgc aac ccc atg ggc ttg caa ctc Ala Val Pro Pro Asp Ser Asp Leu Cys Asn Pro Met Gly Leu Gln Leu 305 310 315	960
aa	962

Fig. 19K

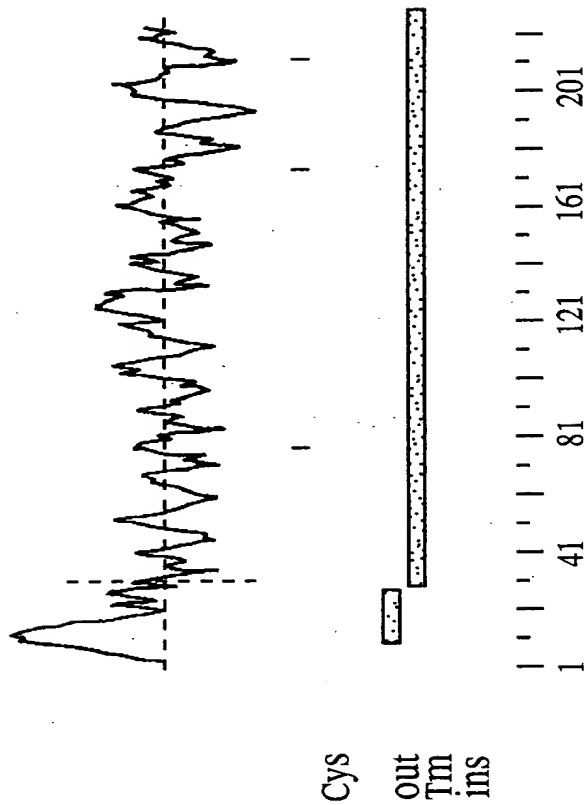


FIG. 19L



Figure 19M

```

M 1 .....PFLFNHLHGLGLRLRLTLDLSSNWLKHISI 30
H 151 HAFHGLRALSHLYLGCNELASFSDHLHGLSATHLLTLDLSSNRLGHISV 200

M 31 PELAAALPTYLKNRLYLHNNPLPCDCSLYHLLRRWHQRLSALHDFEREY 80
H 201 PELAAALPAFLKNGLYLHNNPLPCDCRLYHLLQRLWHQRLSAVRDFAREYV 250

M 81 CLVFKVSESRRVFFEHRSRVFKNCVAAAPGLELPEEQHQAQVGSRLRFC 130
H 251 CLAFKVPASRRVFFQHRSRVFENCSSAPALGLKRPEEHLYALVGRSLRLYC 300

M 131 NTSVPATRVAVWSPKNELLVAPASQDGSIAVLADGSLAIGRVQEQHAGVF 180
H 301 NTSVPAMRIA WSPQQELLRAPGSRDGSIAVLADGSLAIGNVQEQHAGLF 350

M 181 VCLASGPRLHHNQTL EYNSVQKARPEPETENTGFTLLGCIVGLVLVLL 230
H 351 VCLATGPRLHHNQTHEYNSVHFPRPEPEAFNTGFTLLGCAVGLVLVLL 400

M 231 YLFAPPCRGCCCHCCQACRNRNCWPRASSPLQELSA.QSSMLSTTPPDAPS 279
H 401 YLFAPPCR...CCRRACPLPLAPNTQAPAPRAEPHKSSVLSTTPPDAPS 446

M 280 RKASVHKHVVFLEPGKKGLNGRVQLAVPPDSDL CNPMGLQL 320
H 447 PQGQASTST..... 455

```

Fig. 19M

																			206/361																			
GTCGACCCACGCGTCCGGCGAACCCAGCGTCCGCCGAC																			ATG	GCC	TGG	ACC	AAG	TAC	CAG	CTG	L	F	L	CTG	10							
A																			G	L	M	L	V	T	G	S	I	N	T	L	S	A	K	W	A	D	N	30
GCC																			GGG	CTC	ATG	CTT	GTT	ACC	GGC	TCC	ATC	AAC	ACG	CTC	TCG	GCA	AAA	TGG	GCG	GAC	AAT	129
F																			M	A	E	G	C	G	G	S	K	E	H	S	F	Q	H	P	F	L	Q	50
TTC																			ATG	GCC	GAG	GGC	TGT	GGA	GGG	AGC	AAG	GAG	CAC	AGC	TTC	CAG	CAT	CCC	TTC	CTC	CAG	189
A																			V	G	M	F	L	G	E	F	S	C	L	A	A	F	Y	L	L	R	C	70
GCA																			GTG	GGC	ATG	TTC	CTG	GGA	GAA	TTC	TCC	TGC	CTG	GCT	GCC	TTC	TAC	CTC	CTC	CGA	TGC	249
R																			A	A	G	Q	S	D	S	S	V	D	P	Q	Q	P	F	N	P	L	L	90
AGA																			GCT	GCA	GGG	CAA	TCA	GAC	TCC	AGC	GTA	GAC	CCC	CAG	CAG	CCC	TTC	AAC	CCT	CTT	CTT	309
F																			L	P	P	A	L	C	D	M	T	G	T	S	L	M	Y	V	A	L	N	110
TTC																			CTG	CCC	CCA	GCG	CTC	TGT	GAC	ATG	ACA	GGG	ACC	AGC	CTC	ATG	TAT	GTG	GCT	CTG	AAC	369
M																			T	S	A	S	S	F	Q	M	L	R	G	A	V	I	I	F	T	G	L	130
ATG																			ACC	AGT	GCC	TCC	AGC	TTC	CAG	ATG	CTG	CGG	GGT	GCA	GTG	ATC	ATA	TTC	ACT	GGC	CTG	429
F																			S	V	A	F	L	G	R	R	L	V	L	S	Q	W	L	G	I	L	A	150
TTC																			TCG	GTG	GCC	TTC	CTG	GGC	CGG	AGG	CTG	GTG	CTG	AGC	CAG	TGG	CTG	GGC	ATC	CTA	GCC	489

Fig. 20A

T	I	A	G	L	V	V	G	L	A	D	L	L	S	K	H	D	S	Q	170	
ACC	ATC	GCG	GGG	CTG	GTG	GTC	GTG	GGC	CTG	GCT	GAC	CTC	CTG	AGC	AAG	CAC	GAC	AGT	CAG	549
H	K	L	S	E	V	I	T	G	D	L	L	I	I	M	A	Q	I	I	V	190
CAC	AAG	CTC	AGC	GAA	GTG	ATC	ACA	GGG	GAC	CTG	TTG	ATC	ATC	ATG	GCC	CAG	ATC	ATC	GTT	609
A	I	Q	M	V	L	E	E	K	F	V	Y	K	H	N	V	H	P	L	R	210
GCC	ATC	CAG	ATG	GTG	CTA	GAG	GAG	AAG	TTC	GTC	TAC	AAA	CAC	AAT	GTG	CAC	CCA	CTG	CGG	669
A	V	G	T	E	G	L	F	G	F	V	I	L	S	L	L	L	V	P	M	230
GCA	GTT	GGC	ACT	GAG	GGC	CTC	TTT	GGC	TTT	GTG	ATC	CTC	TCC	CTG	CTG	CTG	CCC	ATG	ATG	729
Y	Y	I	P	A	G	S	F	S	G	N	P	R	G	T	L	E	D	A	L	250
TAC	TAC	ATC	CCC	GCC	GGC	TCC	TTC	AGC	GGA	AAC	CCT	CGT	GGG	ACA	CTG	GAG	GAT	GCA	TTG	789
D	A	F	C	Q	V	G	Q	Q	P	L	I	A	V	A	L	L	G	N	I	270
GAC	GCC	TTC	TGC	CAG	GTG	GGC	CAG	CAG	CCG	CTC	ATT	GCC	GTG	GCA	CTG	CTG	GGC	AAC	ATC	849
S	S	I	A	F	F	N	F	A	G	I	S	V	T	K	E	L	S	A	T	290
AGC	AGC	ATT	GCC	TTC	TTC	AAC	TTC	GCA	GGC	ATC	AGC	GTC	ACC	AAG	GAA	CTG	AGC	GCC	ACC	909
T	R	M	V	L	D	S	L	R	T	V	V	I	W	A	L	S	L	A	L	310
ACC	CGC	ATG	GTG	TTG	GAC	AGC	TTG	CGC	ACC	GTT	GTC	ATC	TGG	GCA	CTG	AGC	CTG	GCA	CTG	969

Fig. 20B

G W E A F H A L A L Q I L G F L I L L I G T 330  
 GGC TGG GAG GCC TTC CAT GCA CTG CAG ATC CTT GGC TTC CTC ATA CTC CTT ATA GGC ACT 1029  
  
 A L Y N G L H R P L L G R L S R G R P L 350  
 GCC CTC TAC AAT GGG CTA CAC CGT CCG CTG CTG GGC CGC CTG TCC AGG GGC CGG CCC CTG 1089  
  
 A E E S E Q E R L L G G T R T P I N D A 370  
 GCA GAG GAG AGC GAG CAG GAG AGA CTG CTG GGT GGC ACC CGC ACT CCC ATC AAT GAT GCC 1149  
  
 S \* 372  
 AGC TGA 1155  
  
 GGTTCCTGGAGGCTTCTACTGCCACCCGGGTGCTCCTTCTCCCTGAGACTGAGGCCACACAGGCTGGTGGCCCCGAA 1234  
 TGCCCTATCCCAAGGCCTCACCCCTGTCCCTGCAGAACCCCGAGGCAGCTGCTGCCACAGAAGATAACAACAC 1313  
 CCAAGTCCTCTTTTCTCACTACCACCTGCAGGGTGGTGTACCCAGCCCCCACAGCCTGAGTGCAGTGCAGACCTC 1392  
 AGCTCTCTGGACCCCTCCTACAGCACTAGAGCTAAATCATGAAGTTGAATTGTAGGAATTTACCACCGTAGTGATCTG 1471  
 AATCATAAACTAGATTATCATAAAAAAAAAAAAAAAAAAGGGCGGCCGC 1518

Fig. 20C

FOFFU"0EFD5260

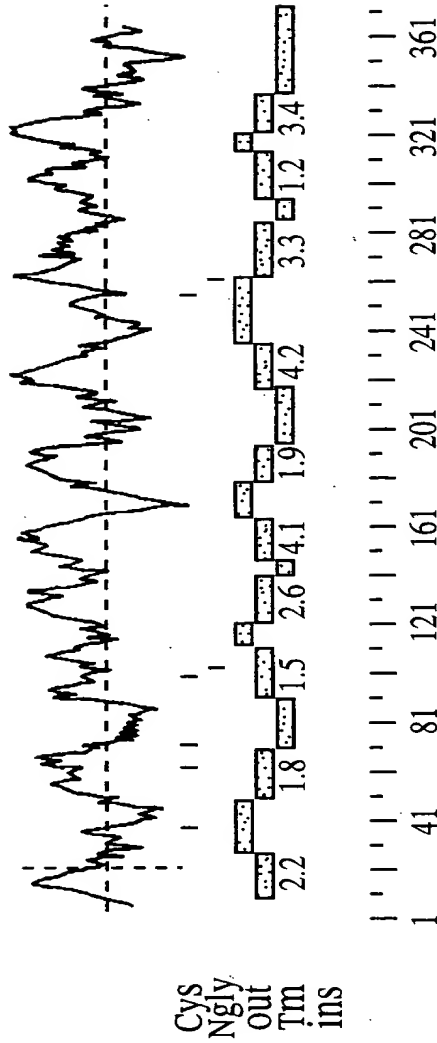


FIG. 20D

# Sequence

210/361

	M	A	P	H	W	
GTCGACCCACGCGTCCCGGACAGCTGGCCTGAAGCTCAGAGCCGGGGCTGGCC	ATG	GCC	CCA	CAC	TGG	5
						72
A V W L L A A R L W G L G I G A E V W						25
GCT GTC TGG CTG CTG GCA AGG CTG TGG GGC CTG GGC ATT GGG GCT GAG GTG TGG TGG						132
N L V P R K T V S S G E L A T V V R R F						45
AAC CTT GTG CCG CGT AAG ACA GTG TCT TCT GGG GAG CTG GCC ACG GTA CGG CGG TTC						192
S Q T G I Q D F L T L T L T E P T G L L						65
TCC CAG ACC GGC ATC CAG GAC TTC CTG ACA CTG ACG CTG ACG GAG CCC ACT GGG CTT CTG						252
Y V G A R E A L F A F S M E A L E L Q G						85
TAC GTG GGC GCC CGA GAG GGC CTG TTT GCC TTC AGC ATG GAG GCC CTG GAG CTG CAA GGA						312
A I S W E A P V E K K T E C I Q K G K N						105
GCG ATC TCC TGG GAG GCC CCC GTG GAG AAG AAG ACT GAG TGT ATC CAG AAA GGG AAG AAC						372
N Q T E C F N F I R F L Q P Y N A S H L						125
AAC CAG ACC GAG TGC TTC AAC TTC ATC CGC TTC CTG CAG CCC TAC AAT GCC TCC CAC CTG						432
Y V C G T Y A F Q P K C T Y V V S A A L						145
TAC GTC TGT GGC ACC TAC GCC TTC CAG CCC AAG TGC ACC TAC GTC GTG AGT GCT GCC CTC						492

Fig. 21A

# LOC101928560

L	P	R	C	P	P	Q	P	A	L	L	T	L	L	W	T	R	G	C	G	165
CTA	CCT	CGG	TGT	CCC	CCC	CAG	CCC	GCC	CTC	CTC	ACC	CTT	CTC	TGG	ACT	CGT	GGA	TGT	GGC	552
P	Q	S	P	A	L	K	H	L	L	I	T	S	L	S	V	L	R	T	C	185
CCA	CAG	AGC	CCT	GCC	CTT	AAG	CAT	CTC	CTC	ATC	ACC	TCT	CTC	TCT	GTC	CTT	AGA	ACA	TGC	612
S	P	S	L	W	S	M	E	S	L	K	M	G	R	A	S	V	P	M	T	205
TCA	CCT	TCA	CTT	TGG	AGC	ATG	GAG	AGT	TTG	AAG	ATG	GGA	AGG	GCA	AGT	GTC	CCT	ATG	ACC	672
Q	L	R	A	M	L	A	F	L	W	M	V	S	C	T	R	P	H	S	T	225
CAG	CTA	AGG	GCC	ATG	CTG	GCC	TTC	TTG	TGG	ATG	GTG	AGC	TGT	ACT	CGG	CCA	CAC	TCA	ACA	732
T	S	W	A	R	N	P	L	S	C	V	T	W	G	P	T	T	P	*		244
ACT	TCC	TGG	GCA	CGG	AAC	CCA	TTA	TCC	TGC	GTA	ACA	TGG	GGC	CCC	ACC	ACT	CCA	TGA		789
AGACAGAGTACCTGGCCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCCTATGTACCTGAGAGTGTGGGCAGCTT																				868
CACGGGGACGACGACAAGTCTACTTCTTCTTCAGGGAGCGGGCAGTGGAGTCCGACTGCTATGCCGAGCAGGTGGTG																				947
GCTCGTGTGGCCCCGTGTCTGCAAGGGCGATATGGGGGGCGCACGGACCCCTGCAGAGGAAAGTGGACCACGTTCTCTGAAGG																				1026
CGCGGCTGGCATGCTCTGCCCCCGAACTGGCAGCTCTACTTCAACCCAGCTGCAGGCGATGCACACCCCTGCAGGACACCTC																				1105

211/361

Fig. 21B

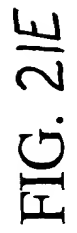
CTGGCACAACACACCTTCTTTGGGGTTTTC AAGCACAGTGGGGTGACATGTACCTGTGCGCCATCTGTAGTACCAG 1184  
 TTGGAAGAGATCCAGCGGGTGTGAGGGCCCCATAAGGAGTACCATGAGGAAGCCAGAAAGTGGGACCGCTACACTG 1263  
 ACCCTGTACCCAGGCCCCCTGGTTGTGATGGCTGCCCAGCCCCGCCCATGCCGGGGCCCTACCACCTGCTTTTCAGAGGAGCAG 1342  
 GGGGCGCGGCTGGCTGCTGAAGGCTACCTTGTGGCTGTCTGTGCAGGCCCGCTCGGTGACCTTGGAGGCCCGGGCCCCCCC 1421  
 TGGAAAACCTGGGGCTGGTGTGGCTGGCGGCTGGTGGCCCTGTGTGCCCTGGTGTCTGTGCTGGTGTCTGTC 1500  
 ATTCGCCCGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAGGCTACTGAGAGGACCTTGGTGTACCCCCCTGGAGCTG 1579  
 CCCAAGGAGCCACACAGTCCCCCCTTCCGGCCCCGTCTCTGAACCAGATGAGAAACTTTGGGATCCTGTCTGGTTACTACT 1658  
 ATTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCCCGGTGCCAGCCCGGTGGGGGCCCCCTTCGCCACCTCCAGG 1737  
 CATCCAGGCCAGCCTCTGCCCTTCTCCAACCTCGGCTTCACCTGGGGGTGGGCGGAACCTCAAATGCCAATGTTACGTG 1816  
 CGCTTACAACCTAGGAGGGAGGACCGGGAGGGCTCGGGCACCCCCCTGCCCTGAGCTCGCGGATGAACCTGAGACGCAAAC 1895  
 TGCAGCAACGCCAGCCACTGCCCGACTCCAACCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGTCGGCGGGA 1974  
 AGCGTGGGAGGTAGCTCCTACTTTTGACACAGGCACCAGCTACCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGG 2053

Fig. 21C



GACAGATACTGCCAGCACCCACCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACTGCCACTTGGTGTGGCTCAC 2132  
 CAGGGCACCGCCTCGCAGAAGGCATCTTCCTCTCTGTGAATCACAGACACGCGGGACCCAGCCGCCAAAACCTT 2211  
 TCAAGGCAGAAAGTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTGTATGTGTGTGCACGC 2290  
 GCGTGCCGCGCTTGTGGCATAGCCCTTCCTGTTTCTGTCAAGTCTTCCCTTGGCCTGGGTCCCTGGTGAGTCATTGGAG 2369  
 CTATGAAGGGGAAGGGTCTGTATCACTTTGTCTCTCTACCCCCACTGCCCCGAGTGTGCGGCACCGATGTACATATGG 2448  
 AGGTGGGGTGGACAGGGTGCTGTGCCCTTCAGAGGGAGTGCAGGGCTTGGGGTGGGCCCTAGTCCTGCTCCTAGGGCTG 2527  
 TGAATGTTTTCAGGGTGGGGGAGGAGATGGAGCCTCCTGTGTGTTTGGGGGAAGGTTGGTGGGGCCTCCCACTTG 2606  
 GCCCCGGGTTCAGTGGTATTTATATACTTGCCCTTCTTCTGTACAGGGCTGGGAAAGGCTGTGTGAGGGGAGAGAAGG 2685  
 AGAGGGTGGGCGCTGCTGTGGACAATGGCATACTCTCTTCCAGCCCTAGGAGAGGGCTCCTAACAGTGTAACTTATTGT 2764  
 GTCCCCGCGTATTATTGTTGTAAATATTTGAGATTTTATATTGA 2811

Fig. 21D





## LOCUS 6340

710 720 730 740 750 760 770  
M ASERTLVYPLELPKEPASPPFRPGPETDEKLWDVPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQP  
H -----W-----GPTP-----  
240

780 790 800 810 820 830  
M LPSPTRLHLGGGRNSNANGYVRLQLGGEDRGSGHPLPELADELRRKLQQRQLPDSNPPESSV  
H -----

Fig. 21H

# Figure 21G

```

360      370      380      390      400      410      420
M QAQWARYTDPVSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPLLVKKNTNF
  ::      ::      .      ...      ::      ::      ...
H ----WTR-----GCGPQ-----SPAL-----KH-----LLI---TSL
160
430      440      450      460      470      480      490
M THVVADRVPGLDGATYTVLFIGTGDGWLKAVSLGPWIHMVEELQVFDQEPVESLVLSQSKKVLFAGSRS
  .      .      .      .      .      .      .
H S-----VLRTCSPSLW-----SMESLKMGRA-----SVPMT
180      190      200
500      510      520      530      540      550      560
M QLVQLSLADCTKYRFCVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVR
::      ::      :      :      :      :      :
H QLRAM-LA-----F-----L-----WMVSCTRPHSTTS-----
210      220
570      580      590      600      610      620      630
M SIPKNITVVSGTDLVLPCHLSSNLAAHAWTFGSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRCYS
  :
H -----W-----
640      650      660      670      680      690      700
M EEQGTRLAAESYLVAVVAGSSVTLEARAPLENGLVWLAVVALGAVCLVLLLVLSLRRRLREELEKGAK
  ::      ::      :      :      :      :
H -----ARNPLS-----CVT-----
230

```

Fig. 21G

Figure 10 "361-403"

```

10      20      30      40      50      60      70
M GGCACGAGGTGCCCGGAGTCAAACGCGAGGGCAGCGCCAGGGATTGGAGCTGCACGAAAGAGGGCTGCTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTC-----GACC-----CACG-----CGTC-----CGCG-----GGACAGCTG
10      20

80      90      100     110     120     130     140
M GACTGAAGTTTAGACCCCTGGGTGTCTGCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAGGGCT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCCTGAAGCTCAGAGCCGGCGGTGCGCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAAGGCT
30      40      50      60      70      80      90

150     160     170     180     190     200     210
M GTGGGGCCCTGGGCATCGGGGCTGAGATGTGGTGAACCTTGTGCCCCGGAAGACAGATATCTTCTGGGGAG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTGGGGCCCTGGGCATTGGGGCTGAGGTGTGGTGAACCTTGTGCCCCGTAAGACAGATGTCTTCTGGGGAG
100     110     120     130     140     150     160

220     230     240     250     260     270     280
M CTGGTCACAGTAGTGAGGCGGTTCTCCCAGACAGGCATCCAGGACTTCCTGACACTGACCCCTGACAGAAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CTGGCCACGGTAGTACGGCGGTTCTCCCAGACCGGCATCCAGGACTTCCTGACACTGACGCTGACGGAGC
170     180     190     200     210     220     230

290     300     310     320     330     340     350
M ATTCTGGCCCTTTATATGTGGGGCCCGAGAGCGGCTGTTTGCCCTTCAGTGTAGAGGCTCTGGAGCTGCA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CCACTGGGCTTCTGTACGTGGGGCCCGAGAGGCCCTGTTTGCCCTTCAGCATGGAGGCCCTGGAGCTGCA
240     250     260     270     280     290     300

```

Fig. 21I



```

710      720      730      740      750      760      770
M TCAAGACAGATACCTGGCTTTTGGCTGAATGAACCCCACTTTGTAGGCTCTGCCCTTGTCCCTGAGAG
   :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGAGCCCTGCCCTTAAGC-----ATCTCCTCATCAC---CTCTCTCTGTCC-TTAGA-
560      570      580      590      600

780      790      800      810      820      830      840
M TGTGGGAAGCTTACGGGAGACGATGACAAGATCTACTTCTTCTCAGTGAGCGGCAGTGGAGTATGAC
   :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----ACATGCTCACCTTCA-CTT-TG-GAGCA---TGGAGAGTTTGA-
610      620      630      640

850      860      870      880      890      900      910
M TGCTATTCCGAGCAGGTGGTGGCTCGTGTGGCGAGAGTCTGTAAGGTGACATGGGGGAGCACGGACGC
   :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGATGG-----GAAGGGCAAGTGTG-----CTATGACCCC
650      660      670

920      930      940      950      960      970      980
M TGCAGAAAGAAATGGACGACGTTCCCTGAAGGCTCGGTGGTGTGCTCAGCCCCCTGACTGGAAGGTCTACTT
   :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H AGCTAAGGGCCATGCTGGCCCTTCTTGT-GGATGGTGAGCTGTACTCGGCCAC--ACT-----CAACAA
680      690      700      710      720      730

990      1000     1010     1020     1030     1040     1050
M CAACCAGCTGAAGCGGTGCACACCCCTCGGGGCGCCTCTTTGGCACAACACCACCTTCTTCGGGTTT
   :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H CTTCCCTG-----GGCA-----CGGAAC-CCA-TTATC-----CTGCG-----TAA
740      750      760      770

```

Fig. 21K



```

1060      1070      1080      1090      1100      1110      1120
M CAAGCGGATGGGGCGATATGGACCTGTCTGCAGTTTGTGAGTACCAGTTGGAACAGATCCAGCAAGTGT
::      :::::      ::      ::::      ::::      :      ::::
H CA-----TGGGGC-----CC--C-----ACCA-----C--TCCA-----
770

1130      1140      1150      1160      1170      1180      1190
M TTGAGGGTCCCTACAAGGAGTACAGTGAAGCCAGAAAGTGGCCCGCTATACTGACCCGGTACCCAG
:::::      ::      :::::      :::::      :      ::      :::      :
H -TGAAG-----ACA--GAGTAC-----CTGGCC--TTTGGCTCAACGAACCTCACTTTGTA---GG
790      800      810      820      830

1200      1210      1220      1230      1240      1250      1260
M CCTCGGCGCTGCTCGTGATCAACAACCTGGCACCAGACAATGGCTACACCAGTTCCCTGGAACCTGCCG
:      ::::::      ::::      ::::      :::::      ::      :      :::::      :
H C--TCTGCCTA-----TGTA-C-----CTGA----GAGT-GTGGGCAGCTTCA---CGGGGGACGAC--
840      850      860      870      880

1270      1280      1290      1300      1310      1320      1330
M GACAACACCCCTCAACTTCATCAAGAAGCACCCCTGATGGAGGACCAGGTGAAGCCTCGGTTGGGCCGCC
:::::      :      :::::::      :::::::      ::::      :::::      :      :::
H GACAAGGTCTACTTCTTTCAGGGAGC-----GGGC--AGTGGAGTC-CGA-----
890      900      910      920

1340      1350      1360      1370      1380      1390      1400
M CCTACTTGTAAGAAGAACTAACTTCACACACGTGTGTGCGCCGACAGGGTCCAGGGCTTGATGGTGC
:::::      ::      ::      :::::      :::::      :      ::      :::
H --CTGCTA-----TGC--CGAGCAGGTGTGGC-----TC-----GTGTGGC
930      940      950

```

Fig. 21L

```

1410      1420      1430      1440      1450      1460      1470
M CACCTATACAGTGTGTTTCATTGGGTACAGGAGATGGCTGGCTGCTGAAGGCTGTGAGCCCTGGGCCCTGG
:  :  .  .  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H C--CGTGTCTG-----CAAGGG--C--GATATGGGGGC-----GCA-----C--GGACCCCTG-
960      970      980      990

1480      1490      1500      1510      1520      1530      1540
M ATCCACATGGTGAGGAACTGCAGGTGTTTGACCAGGAGCCAGTGGAAGTCTGGTGTCTCTCAGAGCA
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H -----GAGGAA-----GTG---GACCACGTTCCTG---AAGGC---GCGG---CTG-GCA
1000     1010     1020     1030

1550      1560      1570      1580      1590      1600      1610
M AGAAGGTGCTCTTTGCTGGCTCCCGCTCTCAGCTGTTTCAGCTGTCTCTGGCCGACTGCACAAAGTACCG
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H -----TGCTCT-----GC-CCCGAACT-GGCAG-CTCTACT-TCA---ACCAGCTGCA---GG---CG
1040     1050     1060     1070     1080

1620      1630      1640      1650      1660      1670      1680
M TTTCTGTAGACTGTGTCCTGGCCAGGACCCTTACTGTGCCTGGAATGTCAACACCAGCCGCTGTGTG
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H ATGC-----ACA---CCCTG--CAGGACACCT-----CCTGGCA---CAACACCACCTTCTTTGGG
1090     1100     1110     1120     1130

1690      1700      1710      1720      1730      1740      1750
M GCCACCACCAAGTGGTCGCTCGGGGTCCTTCTGGTCCAACATGTGGCGAACTTGGACACTTCAAAGATGT
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H GTTT--TTCAA-----GCACAGTGG-----GGT--GACATGTACCTGTC---GGC-CATCTG---TGA
1140     1150     1160     1170

```

Fig. 21M

Sequence

```

1760      1770      1780      1790      1800      1810      1820
M GTAACCAAGTATGGCATTAATAAAGTCAGATCTATTCCCAAGAACAATCACCGTTGTGTGTCAGGCACAGACCT
::: ::::: :::      ::: :::::      ::: :::      ::: :::
H GTA-CCAGT-TGG-----AAG--AGATC-----CAGCG--GGTGTTTGAGG-----
1180      1190      1200      1210

1830      1840      1850      1860      1870      1880      1890
M GGTCCTACCCCTGCCACCTCTCGTCCAAATTGGCCCATGCCCACTGGACCTTCGGAAGCCAGGACCTGCCT
:::      :::      :::      :::      :::      :::      :::
H -----GCC-----CCTATAAGGA--GTACC--ATGA-----GGAAGC-----CCA
1220      1230      1240

1900      1910      1920      1930      1940      1950      1960
M GCAGAACAACCTGGCTCCTTTCTTTATGACACGGGACTCCAGGCGCTGGTGTGATGGCCGCACAGTCCC
: ::::: ::::: ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GAAGTGGGACC--GCTAC--ACT---GACCCCTGTAC-CCAGGCCCTGGTTGTGTGATGGCTGCCCCAGCCCC
1250      1260      1270      1280      1290      1300

1970      1980      1990      2000      2010      2020      2030
M GTCACCTCTGGACCCCTATCGTTGCTATTTCAGAGGAGCAGGGGACAAGACTGGCTGCAGAAAGTACCTTGT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCCATGCCGGGGCCCTACCACTGCTTTTCAGAGGAGCAGGGGCGCGGCTGGCTGCTGAAGGCTACCTTGT
1310      1320      1330      1340      1350      1360      1370

2040      2050      2060      2070      2080      2090      2100
M TGCTGTCTGGCCGGCTCGTCTGGTGACACTGGAGGCACGGGCTCCCTTGGAAACCTGGGGCTCGTGTGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GGCTGTCTGGCAGGCCCGCTCGGTGACCTTGGAGGCCCGGGCCCCCTGGAAACCTGGGGCTGGTGTGG
1380      1390      1400      1410      1420      1430      1440

```

**Fig. 21N**

**Fig. 210**

Figure 21P

```

2460      2470      2480      2490      2500      2510      2520
M CTCAAATGCCAATGGTTATGTGCGTTTACAGTTGGCGGAGAGGACCGAGGAGGATCTGGGCACCCACTG
      :::::::::::::::::::: :::: :::::::::::::::::::: :::::::::::::: ::
H CTCAAATGCCAATGGTTACGTGCGCTTACAACCTAGGAGGGAGGACCGGGAGGGCTCGGGCACCCCTG
1800      1810      1820      1830      1840      1850      1860

2530      2540      2550      2560      2570      2580      2590
M CCTGAGCTCGCGGATGAATTACGACGGAACTACAACAGCGCCAGCCGCTGCCTGACTCCAACCCAGAGG
      :::::::::::::::::::: :::: :::::::::::::::::::: :::::::::::::: ::
H CCTGAGCTCGCGGATGAACCTGAGACGCAAACTGCAGCAACGCCAGCCACTGCCCGACTCCAACCCCGAGG
1870      1880      1890      1900      1910      1920      1930

2600      2610      2620      2630      2640      2650
M AGTCTTCAGTATGAGGGACCCCCCACCCTCATTTGGCGGGGGGGTCTCATGGGAGGTGCA-CTCTTAA
      :::::::::::::::::::: :::: :::::::::::::::::::: :::::::::::::: ::
H AGTCATCAGTATGAGGGGAACCCCC-ACCGCGTCGGCGGGAAG-----CGTGGGAGGTGTAGCTCCTA-
1940      1950      1960      1970      1980      1990

2660      2670      2680      2690      2700      2710      2720
M CTTTGCACAGGCACCACTACCTCAGGGACATGGCAGGGGCACTTGCTCTGCTGCTGGGACAGACACTGCC
      :::::::::::::::::::: :::: :::::::::::::::::::: :::::::::::::: ::
H CTTTGCACAGGCACCACTACCTCAGGGACATGGCAGGGGCACTGCTCTGCTGCTGGGACAGATACTGCC
2000      2010      2020      2030      2040      2050      2060

2730      2740      2750      2760      2770      2780      2790
M CATCATTTGCCCGCGCGTGAGGACCTGCTC-----AGCATGGGCACTGCCACTTGGTGTGGCTCACCAGG
      :: :: :::::::::::::::::::: :::: :::::::::::::::::::: :::::::::::::: ::
H CAGCACCCACCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACTGCCACTTGGTGTGGCTCACCAGG
2070      2080      2090      2100      2110      2120      2130

```

Fig. 21P

# Figure 21Q

```

2800      2810      2820      2830      2840      2850      2860
M ACTTCAGCCTCACAGGAGACA-CACCCCTCCTCT--GTGAATTGAGACATGTGGACCCAGAGCCAAA
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCACCAAGCCTCGCAGAAAGGCATCTTCCTCCTCTCTGTGAATCACAGACACGCGGACCCAGCCGCCAAA
2140      2150      2160      2170      2180      2190      2200

2870      2880      2890      2900      2910      2920
M ACTTTGCAAGGAAGAGGTTTCAAGATGTGGCGGTGTTTGTGCAT--ATATGTGTTGGTATGCATGTGGAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ACTTTTCAAGGCAGAAAGTTTCAAGATGTGTGTTGTTGCTGTATTTGCACATGTGTTGTGTGTGTAT
2210      2220      2230      2240      2250      2260      2270

2930      2940      2950      2960      2970      2980      2990
M GAATGTGTGTGTGTGTG---TGTTGTGTAACTTTCCTGTCTCTATCACGTCTTCCCTTGGCCTGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTGTGTGTGCACGCGGTGCGCGCTTGTGGCATAGCCTTCCCTGTTTCTGTCAAGTCTTCCCTTGGCCTGG
2280      2290      2300      2310      2320      2330      2340

3000      3010      3020      3030      3040      3050      3060
M GGTCCCTCCTGGTTGAGTCTTTGGAGCTATGAAGGGGAAGGGGTCTATAGCACTTTGCTTCTCCTACCCCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H G-TCCTCCTGGT-GAGTCATTGGAGCTATGAAGGGGAAGGGG-TCGTATCACTTTGTCTCTCCTACCCCC
2350      2360      2370      2380      2390      2400      2410

3070      3080      3090      3100      3110      3120      3130
M AGCTGTCCCAAGCTTTGGGCAGTGATGTACATACGGGAAGGAAGGACAGGGTGTGTACCCCTTTTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H A-CTGCCCCGAG-TGTCGGGCAGCGATGTACATATGAGGTGGGGTGGACAGGGTGTGTGCCCCCTTCAG
2420      2430      2440      2450      2460      2470      2480

```

**Fig. 21Q**

```

3140      3150      3160      3170      3180      3190      3200
M GGGAGTCCGGGACTCGGGGTGGCCCTAGCCCTGCTCCTAGGGCTGTGAATGTTTCAGGGCGGGGTT
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H AGGAGTGCAGGGCT-TGGGTGGCCCTAGTCTGCTCCTAGGGCTGTGAATGTTTCAGGGTGGGGGA
2490      2500      2510      2520      2530      2540      2550

3210      3220      3230      3240      3250      3260      3270
M GGGGTGGAGATGGAACCTCCTGC--TTCAGGGGAGGGGTGGCAGGGCCTCCCACTTGCCCTCCGGG
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GGG-----AGATGGAGCCCTCCTGTGTGTTTGGGGGAAGGTGGGTGGGCTCCCACTTGCCCCCGGGG
2560      2570      2580      2590      2600      2610

3280      3290      3300      3310      3320      3330
M TTCGGTGGTATTTTATATTTCGGCTCTTC-TG-ACAGGCTGGGAAGG--TTGTTGGGGAGGGAAGGG
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H TTCAGTGGTATTTTATACTTGCCTTCTTCCTGTACAGGCTGGGAAAGGCTGTGTGAGGGGAGAGAAGGG
2620      2630      2640      2650      2660      2670      2680

3340      3350      3360      3370      3380      3390      3400
M AGGAGTGGGCATGCTATGGATACTGGCCCTATCCTCTCCCTGCTCTGGGAAAAGGGCT--AACAGTGTA
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H AGAGGTGGGCCCTGCTGTGGACAATGGCATACTCTCTCCAGCCCTAGGAGAGGGCTCCTAACAGTGTA
2690      2700      2710      2720      2730      2740      2750

3410      3420      3430      3440      3450      3460      3470
M ACTTATGTGTCCCCACATATTATTGTTGTAAATATTGAGTATTTTATATATGACAAATAAAATGGA
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ACTTATGTGTCCCGCGTATTATTGTTGTAAATATTGAG-ATTTTATATGA-----
2760      2770      2780      2790      2800      2810

```

Fig. 21R

GTCGACCCACGCGTCCGCGGACGCGTGGCGCGCGGGGCCATCCAGACCCCTGCGGAGAGCGGCCGAGCGTGGCC	79
GAGGTTTGAGGGCGCGGAGACCGAGGGCCTGGCGGCGGAAAGAACCGCCCCAAGAGAGCCTCTGCCCCGGGGGCTGC	158
TGGAACATGTGCGGGGGACACAGTTTGTGACAGTTGCCAGACT ATG TTT ACG CTT CTG GTT CTA CTC	228
S Q L P T V T L G F P H C A R G P K A S	28
AGC CAA CTG CCC ACA GTT ACC CTG GGG TTT CCT CAT TGC GCA AGA GGT CCA AAG GCT TCT	288
K H A G E E V F T S K E E A N F F I H R	48
AAG CAT GCG GGA GAA GAA GTG TTT ACA TCA AAA GAA GAA GCA AAC TTT TTC ATA CAT AGA	348
R L L Y N R F D L E L F T P G N L E R E	68
CGC CTT CTG TAT AAT AGA TTT GAT CTG GAG CTC TTC ACT CCC GGC AAC CTA GAA AGA GAG	408
C N E E L C N Y E E A R E I F V D E D K	88
TGC AAT GAA GAA CTT TGC AAT TAT GAG GAA GCC AGA GAG ATT TTT GTG GAT GAA GAT AAA	468
T I A A F W Q E Y S A K G P T T K S D G N	108
ACG ATT GCA TTT TGG CAG GAA TAT TCA GCT AAA GGA CCA ACC ACA AAA TCA GAT GGC AAC	528

Fig. 22A



229/361

R E K I D V M G L L T G L I A A G V F L 128  
AGA GAG AAA ATA GAT GTT ATG GGC CTT CTG ACT GGA TTA ATT GCT GCT GGA GTA TTT TTG 588

V I F G L L G Y Y L C I T K C N R L Q H 148  
GTT ATT TTT GGA TTA CTT GGC TAC TAT CTT TGT ATC ACT AAG TGT AAT AGG CTA CAA CAT 648

P C S S A V Y E R G R H T P S I I F R R 168  
CCA TGC TCT TCA GCC GTC TAT GAA AGG GGC AGG CAC ACT CCC TCC ATC ATT TTC AGA AGA 708

P E E A A L S P L P P S V E D A G L P S 188  
CCT GAG GAG GCT GCC TTG TCT CCA TTG CCG CCT TCT GTG GAG GAT GCA GGA TTA CCT TCT 768

Y E Q A A V A L T R K H S V S P P P Y P 208  
TAT GAA CAG GCA GTG GCG CTG ACC AGA AAA CAC CAC AGT GTT TCA CCA CCA CCA TAT CCT 828

G H T K G F R V F K K S M S L P S H \* 227  
GGG CAC ACA AAA GGA TTT AGG GTA TTT AAA AAA TCT ATG TCT CTC CCA TCT CAC TGA 885

CTACCTTGTCATTTTGGTATAAGAAATTTGTGTTATTTGATAGCCGGGCATGGTGGCTCATGCCTGTATCCCAGCAC 964

TTTGGGAGGCCAGGAGTTCGAGAGCCAGCCCTGGCCCAACATGGTGAAACCCGGTCTCTACTAAAAATTCAAAAATTACCTA 1043

GGCGTCATGGGGCATGCCCTGTAGTCCCACTACTTGGAGGCTGAAGCAGGAGAATTGCTCGAACCTGGAGGCAGAGG 1122

Fig. 22B

TTGCAGTAAGCTGAGATCACGCCACTGCATTCAGCCTGGCGACAGAGCAAGACTCCATCTCAAAAATAAAAAA 1201  
AAGAAAGAAAGAAAGAAAGAAAGAGAGATGAAGGAGGAGGAGGAGGAGAAAGGAGAAAGAA 1280  
GAAGAAAGAACCCACAAAAGACATGACTATCCAACCTTTTATGACAAACTGCAAGGAATAAGGAAATAAGTCCATG 1359  
TACTGTACCCACAGAAGTTCTGTCTGCATCTTGGACCTGAACTTGATCATTTATCAGCTTGATAAGAGACTTTTGTACTCT 1438  
ATATCCTTGCAGTTAAGAAAGAAAGCACTTTTGTAAATGTTTAAATGGTTCAAAAAAAATCTTCTTATAAAGAG 1517  
CATAGGTAGAAATTAGTGAACCTCTTTGGATCCTTTGTACAGATAAAGGTTATAGATTTCTTGTGTTGAATATTAAAAAAG 1596  
CAAGGATGCTAACCATTAAAGATTATCCAAAGTCAGGCTGGCGCAGTGGCTCACGCCCTGTAATCCCAGCACTTTGGGA 1675  
GGGATAGGTGGCGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAAACATGGCAAAACCCCGTCTCTACAAAA 1754  
ATACAAAAGAAAATTAGCCAGACATGATGGCGGGTGCCCTCTAATCCCAGCTACTGGGAGGCTGAGGTGGGAGAAATCGCT 1833  
TGAACTCGGGAGGTGAGGTTGTAGTGAGCGGAGATTGTGCCATTGCACCTCCAACCTGGCGCACAGAGTGAGACTCCAT 1912  
CTCAAAAATAAAAAATAAGATTATCCAAAATAAGATAATTGGACCTACTCTTTCTTAGGATTTTTTGGCGGGGGT 1991  
TAGAAATAC TTCACAGAAATTGACAT TTCAGTATAAATCTGTGACCTTAATAATAATCACTTGGTTTATATGTTAAATT 2070  
ATTGCACAGCAGTCATCATATTTTGCAGAGTTTAGTTCTTAACCTCTTGCTGCAGTCATGTTTATTATAGGTAGTGGG 2149  
GTCAGTAGTTTCTTCTTAAAAAATACTATTTGCTATGAAGTTAGTTCTTCAGAAGATACAAAGTTTGCAATGAAAAAG 2228  
GATTTGCAAGGGTTGTTATGCTATCAAAATAACACAGACCTAAAACTAGGAGACACTAGAACCTTAATGAAGTTGCCCTG 2307  
TTACTGATTTAGTAAATACTCCCATCTTCGTTGCAAAATTATCTCTGTATAACTACATATGATTTTGAATAATTGT 2386  
TAAACTTCATAAGTAATAGTTTGAGAAATGTGAAAAAGTAATTTGCTTTTCTGCTCTTAAAAATAATATTGATTAATGTT 2465  
ACCAGAAAAATAAAAAATAAAAAAGGCGGGCCG 2498

**Fig. 22C**

102110-0610500

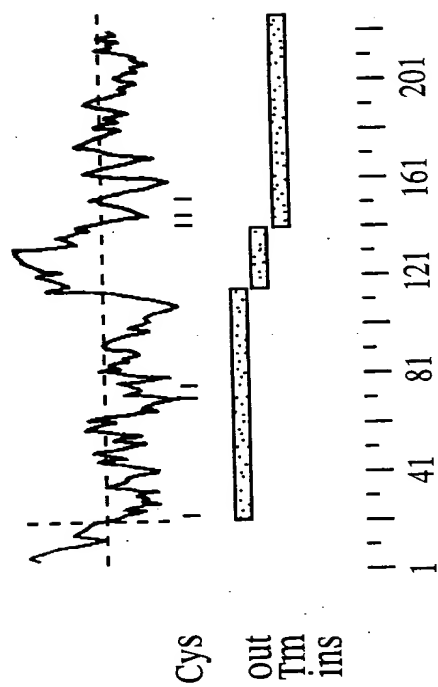


FIG. 22D

GTCGACCCAC	GGTCCGCTG	CGTTCTCACC	CCTGGACCAC	CCTGGGAGAA	CAGTTGACCG	60
AAGTTTGTTT	GGCAGTTGCT	GCTGGACT	ATG TTT CTG	CTT CTG	GTA CTC	112
	Met	Phe	Leu	Leu	Val Val Leu	
	1				5	
AGC CAG CTG	CCC AGA CTT	ACC CTC	GCG GTT	CCT CAT	ACA AGA AGC CTA	160
Ser Gln Leu	Pro Arg Leu	Thr Leu	Ala Val	Pro His	Thr Arg Ser Leu	
	10				20	
AAG AAT TCT	GAA CAT GCC	CCA GAA	GGA GTC	TTT GCA	TCA AAA AAA GCA	208
Lys Asn Ser	Glu His Ala	Pro Glu	Gly Val	Phe Ala	Ser Lys Lys Ala	
	25				35	
					40	
GCA AGC ATC	TTT ATG CAC	CGT CGC	CTC CTA	TAC AAT	AGA TTT GAT TTA	256
Ala Ser Ile	Phe Met His	Arg Arg	Leu Leu	Tyr Asn	Arg Phe Asp Leu	
	45				55	
GAA CTC TTC	ACT CCC GGG	AAC CTG	GAG AGA	GAG TGC	TAT GAG GAG TTC	304
Glu Leu Phe	Thr Pro Gly	Asn Leu	Glu Arg	Glu Cys	Tyr Glu Glu Phe	
	60				70	
					65	
TGT AGT TAT	GAA GAA GCC	AGA GAG	ATC CTC	GGG GAC	AAC GAA GAA ATG	352
Cys Ser Tyr	Glu Glu Ala	Arg Arg	Glu Ile	Leu Gly	Asn Glu Glu Met	
	75				85	
					80	

Fig. 22E

Sequence Alignment

ATC ACA TTC TGG CGG GAA TAT TCA GTC AAA GGA CCA ACC ACA AGA TCA	400
Ile Thr Phe Trp Arg Glu Tyr Ser Val Lys Gly Pro Thr Thr Arg Ser	
90	100
GAT GTC AAC AAA GAG AAA ATT GAT GTT ATG GGC CTT CTG ACT GGC TTA	448
Asp Val Asn Lys Glu Lys Ile Asp Val Met Gly Leu Thr Gly Leu	
105	115
ATT GCG GCT GGA GTA TTC TTG GTT GTT TTT GGC TTA CTT GGT TAC TAT	496
Ile Ala Ala Gly Val Phe Leu Val Val Phe Gly Leu Gly Tyr Tyr	
125	135
CTG TGT ATC ACC AAG TGT AAT AGG CAG CCA TAT CAA GGT TCT TCA GCT	544
Leu Cys Ile Thr Lys Cys Asn Arg Gln Pro Tyr Gln Gly Ser Ser Ala	
140	150
GTC TAC ACA AGA AGG ACC AGG CAC ACA CCG TCC ATC ATT TTC AGA ACC	592
Val Tyr Thr Arg Arg Thr Arg His Thr Pro Ser Ile Ile Phe Arg Thr	
155	165
CAT GAG GAA GCT GTC TTG TCT CCA TCG TCA TCC TCA GAG GAC GCG GGA	640
His Glu Glu Ala Val Leu Ser Pro Ser Ser Ser Ser Glu Asp Ala Gly	
170	180

Fig. 22F

CTA CCT TCC TAT GAA CAG GCA GTA GCT CTG ACC AGA AAA CAC AGT GTC 688  
 Leu Pro Ser Tyr Glu Gln Ala Val Ala Leu Thr Arg Lys His Ser Val 200  
 185 190 195

TCA CCA CCA CCT CCA TAT CCT GGG CCA GCA AAA GGA TTT AGG GTA TTT 736  
 Ser Pro Pro Pro Tyr Pro Gly Pro Ala Lys Gly Phe Arg Val Phe 215  
 205 210

AAA AAG TCA ATG TCA CTC CCA TCT CAC TAAGCCCACC TTGCCGCCTT 783  
 Lys Lys Ser Met Ser Leu Pro Ser His 225  
 220

GCTGTGGTCT GAATAATATG TTCTTCCTGA AACAAACAACA ACAAAAAAAT TTGCCCTGTTT 843  
 AGCTTTTAT GACAAAGCAC AAGGAATAAA GGAACACTAT ATACAGAACA GAATTCACCA 903  
 CAGCCCCGCT TTCAGCTCTG CCCCCAACTG GATTGCTGTC TTGGTAAGAG ACTTCTACCG 963  
 TGCTTCCTCG AAGTTAAGAA GAAAGTGCCT TTTTGCAATG TAAACTGTAC TGGTCAAAC 1023  
 ATTCTTGCTA CAGCTAGGTA CCTATAATCC CCACCTTCAG GAGACTTAGG CGGGAGGGAT 1083  
 GAGAGTTCAA GGCCAGCCTG GGCCCTGTCA GGACGCTGTC TCAAAACAATA GTTTGTTATC 1143  
 AATAGAATAA TTAGAATTAA CAAACTAGGA TTTTCAGTCT TAAGTCATGA TATTGGATCT 1203  
 TCTCTTCAGT AAGGTTTCTT TTTGGCTAGA AATACTTCAT AGAATTGAC ATTTTGGTAT 1263  
 ACATCTGTGG CCTTGATACA ATGACTTGAT TTTCTGTTTT AATTAGTGCA GAGGATTCAG 1323  
 CAAATTTGCA GGTCTTCATT TTGTTCCCTC GCTATCCATC GATCATGTTT CAGTGTATTA 1383  
 AGAGGAGTCA GCCAGGCGTG GTGGCCACAC CCTGTGATCC CAGCACTTAG GGGGCGATAG 1443  
 GCAGGCAGAT CTCTGTGAGC TGAAGGACAG CCTGGCCCTAC AAAGTCCAGG ACAACCCGAGA 1503  
 CCACACAGAG AAACCTTGTC TTGAAAAACA AAACAAAAAC AAGAGAGAGA GAGAGAGAGA 1563

Fig. 22G

GAGAAAAGAG ATGTCAAGAG GTTTTGTGTT TTTT TTTT AAATTACTAT TTATGGGCCT 1623  
CACTTGGAAA AGTGCTTGCC ATGCAAAATAG AAGGACAGGA GTTCAATCCT CATTACCCAC 1683  
ATTTGAAACA AATAACAAGA AAAACAAACC AAAAACCAC AACAACAAA ATCTTGAGAA 1743  
CTTGAGTGAA TACCGGTAAC CTCAGGGCTA GGCACGTGTA CTGAATCAGG AGCCTCCAGA 1803  
TCCAGGGAAA CGCTGTCTCA ACAAATAAAT AAATAAGTAA GTCAGTGAGG TGGTCTTTAA 1863  
ACCCAGCACT TGAGAGCCAA AGCAGGGCAG AGCTCAGTGA GTTGGAGACC AGCCTGGTCT 1923  
ACAAAGCAAG TTCTAAGGA GCCAGGGCAC AGAGAAACCC TGTCTGAAGG AAAAAA AAAA 1983  
AAAAAAAAG GCGGCGCGC 2002

**Fig. 22H**

G	1	ATGTTTCTGCTTCTGGTGGTACTCAGCCAGCTGCCCCAGACTTACCCCTCGC	50
H	1	ATGTTTACGCTTCTGTTCTACTCAGCCAACTGCCCCACAGTTACCCCTGGG	50
G	51	GGTTCCCTCAT...ACAAGAAGCCCTAAAGAATTCTGAACATGCCCCCAGAAG	97
H	51		
G	98	GAGTCTTTGCATCAAAAAGCAGCAAGCATCTTTATGCACCGTCGCCTC	147
H	101	AAGTGTTTACATCAAAAAGAGAGCAAACTTTTTCATACATAGACGCCTT	150
G	148	CTATACAATAGATTGATTTAGAACTCTTCACTCCCGGGAACCTGGAGAG	197
H	151	CTGTATAATAGATTGATCTGGAGCTCTTCACTCCCGGCAACCTAGAAAAG	200
G	198	AGAGTGCTATGAGGAGTTCTGTAGTTATGAAGAAGCCAGAGAGATCCCTCG	247
H	201	AGAGTGCAATGAAGAACTTTGCAATTATGAGGAAGCCAGAGAGATTTTGTG	250

Fig. 22I



G	248	GGGACAAACGAAAGAAATGATCACATTCCTGGCGGGAATATTCAGTCAAAGGA	297
H	251	TGGATGAAGATAAAACGATTGCATTTTGGCAGGAATATTCAGCTAAAGGA	300
G	298	CCAACCACAGATCAGATGTCAACAAGAGAAAAATTGATGTTATGGGCCT	347
H	301	CCAACCACAAAAATCAGATGGCAACAGAGAGAAAAATAGATGTTATGGGCCT	350
G	348	TCTGACTGGCTTAATTGCGGCTGGAGTATTCCTGGTTGTTTGGCCTTAC	397
H	351	TCTGACTGGATTAAATTGCTGCTGGAGTATTTTGGTTATTTTGGATTAC	400
G	398	TTGGTTACTATCTGTGTATCACCAGTGTAATAGGCAGCCATATCAAGGT	447
H	401	TTGGCTACTATCTTTGTATCACTAAGTGTAATAGGCTACAACATCCATGC	450
G	448	TC TTCAGCTGTCTACACAAGAGGACCAGGCACACACCGTCCATCATTTT	497
H	451	TC TTCAGCCGCTCTATGAAAGGGG...AGGCACACTCCCTCCATCATTTT	497

Fig. 22J

G	498	CAGAACCCATGAGGAAGCTGTCTTGTCTCCAT...CGTCATCCTCAGAGG	544
H	498	CAGAAGACCTGAGGAGGCTGCCTTGTCTCCATTGCCGCCCTTCTGTGGAGG	547
G	545	ACGCGGGACTACCTTCCTATGAACAGGCAGTAGCTCTGACCAGAAACAC	594
H	548	ATGCAGGATTACCTTCTTATGAACAGGCAGTGGCGCTGACCAGAAACAC	597
G	595	AGTGCTCACCACCCACCTCCATATCCTGGGCCAGCAAAAGGATTTAGGGT	644
H	598	AGTGTTTCACCACCCACCATATCCTGGGCACACAAAAGGATTTAGGGT	647
G	645	ATTAAAAAGTCAATGTCACTCCCATCTCAC	675
H	648	ATTAAAAAATCTATGTCTCTCTCCCATCTCAC	678

Fig. 22K

G 1 MFLLLVLSQLPRLTLAVPH.TRSLKNSEHAPEGVFASKKAASIFMHRRL 49  
 || |||.|||||.|| || || |||.|||||.|||.|||.|||.|||.|||  
 H 1 MFTLLVLSQLPTVTLGPPHCARGPKASKHAGEEVFTSKEEANFFIHRRL 50  
 G 50 LYNRFDELFTPGNLERECYEEFCSEYEEAREILGDNEEMITFWREYSVKG 99  
 ||||| ||||| ||||| |||.||||| | :. | ||. || | |  
 H 51 LYNRFDELFTPGNLERECNEELCNYEEAREIFVDEDKTIAFWQEYSAKG 100  
 G 100 PTTSDVNKEKIDVMGLLTGLIAAGVFLVFGLLGYLCLITKCNRPYQG 149  
 |||: || | : ||||| ||||| ||||| : ||||| ||||| :  
 H 101 PTTKSDGNREKIDVMGLLTGLIAAGVFLVIFGLLGYLCLITKCNRLQHPC 150  
 G 150 SSAVYTRRTRHTPSIIFRTHHEEAVLSP.SSSSEDAGLPSYEQAVLTRKH 198  
 |||| | ||||| || | || | ||||| ||||| ||||| |||||  
 H 151 SSAVY.ERGRHTPSIIFRRPEEAALSPLPPSVEDAGLPSYEQAVLTRKH 199  
 G 199 SVSPPPPPYGPAGKGFVRVFKKMSMLPSH 225  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 H 200 SVSPPPPPYPGHTKGFRVFKKMSMLPSH 226

Fig. 22L

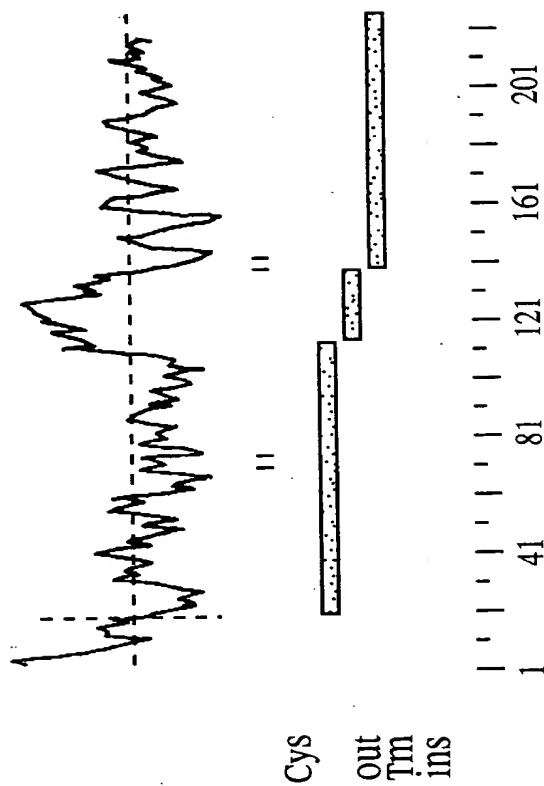


FIG. 22M



T	Y	G	P	D	C	L	A	C	Q	G	G	S	Q	R	P	C	S	G	N	151
ACC	TAC	GGT	CCC	GAC	TGT	CTC	GCA	TGC	CAG	GGC	GGC	TCC	CAG	AGG	CCC	TGC	AGC	GGG	AAT	566
G	H	C	S	G	D	G	S	R	Q	G	D	G	S	C	R	C	H	M	G	171
GGC	CAC	TGC	AGC	GGA	GAT	GGG	AGC	AGA	CAG	GGC	GAC	GGG	TCC	TGC	CGG	TGC	CAC	ATG	GGG	626
Y	Q	G	P	L	C	T	D	C	M	D	G	Y	F	S	S	L	R	N	E	191
TAC	CAG	GGC	CCG	CTG	TGC	ACT	GAC	TGC	ATG	GAC	GGC	TAC	TTC	AGC	TCG	CTC	CGG	AAC	GAG	686
T	H	S	I	C	T	A	C	D	E	S	C	K	T	C	S	G	L	T	N	211
ACC	CAC	AGC	ATC	TGC	ACA	GCC	TGT	GAC	GAG	TCC	TGC	AAG	ACG	TGC	TCG	GGC	CTG	ACC	AAC	746
R	D	C	G	E	C	E	V	G	W	V	L	D	E	G	A	C	V	D	V	231
AGA	GAC	TGC	GGC	GAG	TGT	GAA	GTG	GGC	TGG	GTG	CTG	GAC	GAG	GGC	GCC	TGT	GTG	GAT	GTG	806
D	E	C	A	A	E	P	P	P	C	S	A	A	Q	F	C	K	N	A	N	251
GAC	GAG	TGT	GCG	GCC	GAG	CCG	CCT	CCC	TGC	AGC	GCT	GCG	CAG	TTC	TGT	AAG	AAC	GCC	AAC	866
G	S	Y	T	C	E	E	C	D	S	S	C	V	G	C	T	G	E	G	P	271
GGC	TCC	TAC	ACG	TGC	GAA	GAG	TGT	GAC	TCC	AGC	TGT	GTG	GGC	TGC	ACA	GGG	GAA	GGC	CCA	926
G	N	C	K	E	C	I	S	G	Y	A	R	E	H	G	Q	C	A	D	V	291
GGA	AAC	TGT	AAA	GAG	TGT	ATC	TCT	GGC	TAC	GCG	AGG	GAG	CAC	GGA	CAG	TGT	GCA	GAT	GTG	986

Fig. 23B

D	E	C	S	L	A	E	K	T	C	V	R	K	N	E	N	C	Y	N	T	311	
GAC	GAG	TGC	TCA	CTA	GCA	GAA	AAA	ACC	TGT	GTG	AGG	AAA	AAC	GAA	AAC	TGC	TAC	AAT	ACT	1046	
P	G	S	Y	V	C	V	C	P	D	G	F	E	E	T	E	D	A	C	V	331	
CCA	GGG	AGC	TAC	GTC	TGT	GTG	TGT	CCT	GAC	GGC	TTC	GAA	GAA	ACG	GAA	GAT	GCC	TGT	GTG	1106	
P	P	A	E	A	E	A	T	E	G	E	S	P	T	Q	L	P	S	R	E	351	
CCG	CCG	GCA	GAG	GCT	GAA	GCC	ACA	GAA	GGA	GAA	AGC	CCG	ACA	CAG	CTG	CCC	TCC	CGC	GAA	1166	
D	L	*																		354	
GAC	CTG	TAA																		1175	
TGT	GCC	GACTT	ACCC	TTT	AAAT	TAT	TCA	GAA	GAT	GTCC	CGTGG	AAAT	GTGG	CCCTG	AGG	ATGCC	GTCTC	CTGC	AGT	1254	
GG	AC	AGCG	GGG	GAG	AGG	CTGC	CTCT	CTA	ACGG	TGAT	TCT	CATT	TGT	CCCTT	AAAC	AGCTG	CAATT	CTTGG	TG	1333	
TTCT	TAA	CAG	ACTT	GTAT	ATTT	TGAT	ACAG	TCTT	TGTA	ATA	AAATT	GAC	CATT	GTA	GGTA	ATCA	AAAA	AAAA	AAAA	1412	
AAAA	AGG	CGG	CGC	GCT	AG	C															1432

Fig. 23C

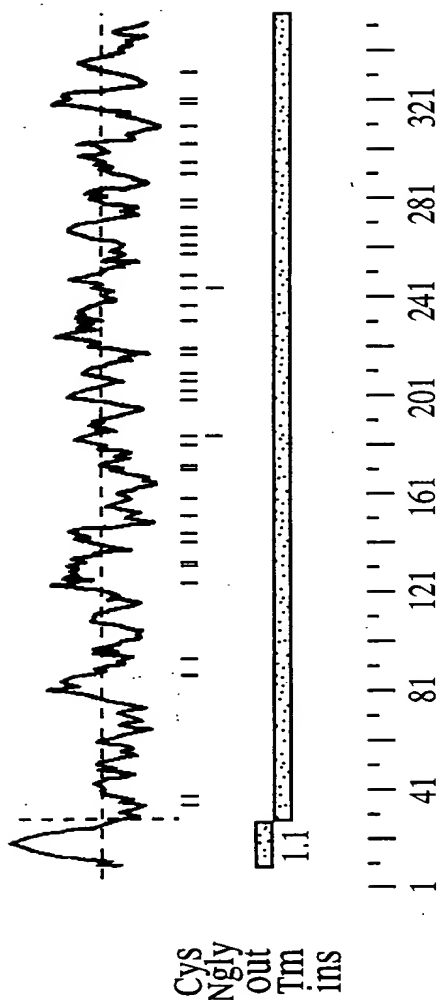


FIG. 23D



H EDL

**Fig. 23E**



260 270 280 290 300 310 320  
C GGCAACACGGCGTGGGAGGAGAAAGAGTCTGTCCAAGTACGAATTCAGTGAGATTCGGCTCCTGGAGATTA  
:: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::  
H GGGAAACACGGCTTGGGAGGAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCCTGCTGGAGATCC  
280 290 300 310 320 330 340  
330 340 350 360 370 380 390  
C TGGAGGGCCTGTGTGACAGCAACGACTTTGAATGCAACCAACT-CTTGGAACAGCATGAGGAGCAGCTAG  
:: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::  
H TGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGC-GCAGGAGGAGCACCTGG  
350 360 370 380 390 400 410  
400 410 420 430 440 450 460  
C AGGCCTGGTGGCAGACACTGAAGAAGGAGTGCCCTAACCTATTGAGTGGTCTGTGTACACACACTGAA  
:: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::  
H AGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTGTGTGAAGACACTGAA  
420 430 440 450 460 470 480  
470 480 490 500 510 520 530  
C AGCATGCTGTCTTCCAGGCACCTATGGGGCCAGACTGTTCAGGAATGCCAGGGTGGGTCTCAGAGGCCCTTGT  
:: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::  
H AGTGTGCTGTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGC  
490 500 510 520 530 540 550

**Fig. 23G**

**Fig. 23H**

C	GCAATGTACAGTACTGTGAAAAATGTCAAACGGCTCCTACACATGTGAAGAGTGATTCTACCTGTGTGGG	820	830	840	850	860	870	880
H	GCCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGG	840	850	860	870	880	890	900
C	CTGCACAGGAAAAGGCCCCAGCCCAATTGTAAAGAGTGTATCTCTGGCTACAGCAAGCAGAAAGGAGAGTGT	890	900	910	920	930	940	950
H	CTGCACAGGGGAAGGCCCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGT	910	920	930	940	950	960	970
C	GCAGATATAGATGAATGCTCATTAGAAACAAGAGTGTGTAAAGGAAAAATGAGAACTGCTACAATACTC	960	970	980	990	1000	1010	1020
H	GCAGATGTGACGAGTGCTCCTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTC	980	990	1000	1010	1020	1030	1040
C	CAGGGAGCTTTGTCTGCGTGTGTCCGGAAGTTTCGAGGAGACAGAAAGATGCTTGTGTACAGACAGCAG	1030	1040	1050	1060	1070	1080	1090
H	CAGGGAGCTACGTCTGTGTGTCTGACGGCTTCGAAGAA-ACGGAAGATGCCTGTGTGCCCGCCGCGCAG	1050	1060	1070	1080	1090	1100	1110

**Fig. 23I**

```

1100      1110      1120      1130      1140      1150
C AAGCGAAGTGGCAGAGGAAAGT--CCC-ACACAGCCACCTCCCATGAGGATTGTGACGGCATCCAG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H AGGCTGAAGCCACAGAGGAGAAAGCCCGACACAGCTGCCCTCCCGGAAGA-----CCTG
1120      1130      1140      1150      1160      1170
1160      1170      1180      1190      1200      1210      1220
C GTTCAGAAGCTGGACTCTCACCCCTTTTAAAGTTATTGAGAGGACATCCTATAGAAAAATGTGCCCCATGGAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H --TAATGTGCCGGAAGCTT--ACCCCTTTAAATATTTCAGAAGGATGTCCCCTGGGAAAAATGTGGCCCTGAGGA
1180      1190      1200      1210      1220      1230

1230      1240      1250      1260      1270      1280      1290
C ATCAACCCCAATTTCTCCAGGAAGTTTGG-AGGAAGAAGCTGCCCTGCTTTGAAACAGTAGATACTCACTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H TGCCGTCTC-----CTGCAGTGGACAGCGCGGGGAGAGGCTGCCCTGCTCTCTAACGGTTGATTCTCATTT
1240      1250      1260      1270      1280      1290      1300
1300      1310      1320      1330      1340      1350      1360
C GGCCCTTTAAACGCTGCATTTCTTGGTGGTCTTAAACAGATTCTGATATTTTGATACTGTTCTTTATA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTCCCTTAAACA-GCTGCATTTCTTGGTGTCTTAAACAGACTTGATATATTTTGATACAGTTCTTTGTA
1310      1320      1330      1340      1350      1360      1370

1370      1380      1390
C ATAAAAATTGATCATTTGAAGGTCACCCAGGA-----CA-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ATAAAAATTGACCAATTGTAGGTAATCAAAAAAATAAAAAAAGGCGCGCGCTAGAC
1380      1390      1400      1410      1420      1430

```

Fig. 23J

# REF ID: A66520

GTCGACCCACGCTCCGTCTGCGGCCCCAGCCCTCTCCTCAGCTCGCGCAGTCTCCGCCCGCAGTCTCAGCTGCAGCTG	79
CAGGACTGAGCCGTGCACCCGGAGAGACCCCGGAGGAGGCGACAACTTCGCAGTGCCGCGACCCCAACCCAGCCCT	158
GGGTAGCCTGCAGC ATG GCC CAG CTG TTC CTG CCC CTG CTG GCA GCC CTG GTC CTG GCC CAG	16 220
A P A A L A D V L E G D S S E D R A F R	36
GCT CCT GCA GCT TTA GCA GAT GTT CTG GAA GGA GAC AGC TCA GAG GAC CGC GCT TTT CGC	280
V R I A G D A P L Q G V L G G A L T I P	56
GTG CGC ATC GCG GGC GAC GCG CCA CTG CAG GGC GTG CTC GGC GGC CTC ACC ATC CCT	340
C H V H Y L R P P P S R R A V L G S P R	76
TGC CAC GTC CAC TAC CTG CTG CGG CCA CCG AGC CGC CGG GCT GTG CTG GGC TCT CCG CGG	251/361 400
V K W T F L S R G R E A E V L V A R G V	96
GTC AAG TGG ACT TTC CTG TCC CGG GGC CGG GAG GCA GAG GTG CTG GTG GCG CGG GGA GTG	460
R V K V N E A A Y R F R V A L P A Y P A S	116
CGC GTC AAG GTG AAC GAG GCC TAC CGG TTC CGC GTG GCA CTG CCT GCG TAC CCA GCG TCG	520
L T D V S L A L S E L R P N D S G I Y R	136
CTC ACC GAC GTC TCC CTG GCG CTG AGC GAG CTG CGC CCC AAC GAC TCA GGT ATC TAT CGC	580

Fig. 24A

# PROTEIN

C	E	V	Q	H	G	I	D	D	S	S	D	A	V	E	V	K	V	K	G	156
TGT	GAG	GTC	CAG	CAC	CAC	GAT	GAT	GAC	AGC	AGC	GAC	GCT	GTG	GAG	GTC	AAG	GTC	AAA	GGG	640
V	V	F	L	Y	R	E	G	S	A	R	Y	A	F	S	F	S	G	A	Q	176
GTC	GTC	TTT	CTC	TAC	TAC	GAG	GGC	TCT	GCC	CGC	TAT	GCT	TTC	TCC	TTT	TCT	GGG	GCC	CAG	700
E	A	C	A	R	I	G	A	H	I	A	T	P	E	Q	L	Y	A	A	Y	196
GAG	GCC	TGT	GCC	CGC	ATT	GGA	GCC	CAC	ATC	GCC	ACC	CCG	GAG	CAG	CTC	TAT	GCC	GCC	TAC	760
L	G	G	Y	E	Q	C	D	A	G	W	L	S	D	Q	T	V	R	Y	P	216
CTT	GGG	GGC	TAT	GAG	CAA	TGT	GAT	GCT	GGC	TGG	CTG	TCG	GAT	CAG	ACC	GTG	AGG	TAT	CCC	820
I	Q	T	P	R	E	A	C	Y	G	D	M	D	G	F	P	G	V	R	N	236
ATC	CAG	ACC	CCA	CGA	CAG	GCC	TGT	TAC	GGA	GAC	ATG	GAT	GGC	TTC	CCC	GGG	GTC	CGG	AAC	880
Y	G	V	V	D	P	D	D	L	Y	D	V	Y	C	Y	A	E	D	L	N	256
TAT	GGT	GTG	GTG	GAC	CCG	GAT	GAC	CTC	TAT	GAT	GTG	TAC	TGT	TAT	GCT	GAA	GAC	CTA	AAT	940
G	E	L	F	L	G	D	P	P	E	K	L	T	L	E	E	A	R	A	Y	276
GGA	GAA	CTG	TTC	CTG	GGT	GAC	CCT	CCA	GAG	AAG	CTG	ACA	TTG	GAG	GAA	GCA	CGG	GCG	TAC	1000
C	Q	E	R	G	A	E	I	A	T	T	G	Q	L	Y	A	A	W	D	G	296
TGC	CAG	GAG	CGG	GGT	GCA	GAG	ATT	GCC	ACC	ACG	GGC	CAA	CTG	TAT	GCA	GCC	TGG	GAT	GGT	1060

Fig. 24B



# GENE "GTF320"

G	L	D	H	C	S	P	G	W	L	A	D	G	S	V	R	Y	P	I	V	316
GGC	CTG	GAC	CAC	TGC	AGC	CCA	GGG	TGG	CTA	GCT	GAT	GGC	AGT	GTG	CGC	TAC	CCC	ATC	GTC	1120
T	P	S	Q	R	C	G	G	G	L	P	G	V	K	T	L	F	L	F	P	336
ACA	CCC	AGC	CAG	CGC	TGT	GGT	GGG	GGC	TTG	CCT	GGT	GTC	AAG	ACT	CTC	TTC	CTC	TTC	CCC	1180
N	Q	T	G	F	P	N	K	H	S	R	F	N	V	Y	C	F	R	D	S	356
AAC	CAG	ACT	GGC	TTC	CCC	AAT	AAG	CAC	AGC	CGC	TTC	AAC	GTC	TAC	TGC	TTC	CGA	GAC	TCG	1240
A	Q	P	S	A	I	P	E	A	S	N	P	A	S	N	P	A	S	D	G	376
GCC	CAG	CCT	TCT	GCC	ATC	CCT	GAG	GCC	TCC	AAC	CCA	GCC	TCC	AAC	CCA	GCC	TCT	GAT	GGA	1300
L	E	A	I	V	T	V	T	E	T	L	E	E	L	Q	L	P	Q	E	A	396
CTA	GAG	GCT	ATC	GTC	ACA	GTG	ACA	GAG	ACC	CTG	GAG	GAA	CTG	CAG	CTG	CCT	CAG	GAA	GCC	1360
T	E	S	E	S	R	G	A	I	Y	S	I	P	I	M	E	D	G	G	G	253/361
ACA	GAG	AGT	GAA	TCC	CGT	GGG	GCC	ATC	TAC	TCC	ATC	CCC	ATC	ATG	GAG	GAC	GGA	GGA	GGT	416
G	S	S	T	P	E	D	P	A	E	A	P	R	T	L	L	E	F	E	T	1420
GGA	AGC	TCC	ACT	CCA	GAA	GAC	CCA	GCA	GAG	GCC	CCT	AGG	ACG	CTC	CTA	GAA	TTT	GAA	ACA	436
Q	S	M	V	P	P	T	G	F	S	E	E	E	G	K	A	L	E	E	E	1480
CAA	TCC	ATG	GTA	CCG	CCC	ACG	GGG	TTC	TCA	GAA	GAG	GAA	GGT	AAG	GCA	TTG	GAG	GAA	GAA	456
																				1540

Fig. 24C

[illegible]

**Fig. 24D**

# REFSEQ

R	T	A	P	A	G	T	S	V	Q	A	Q	P	V	L	P	T	D	S	A	636
AGA	ACT	GCC	CCA	GCA	GGG	ACC	TCA	GTG	CAG	GCC	CAG	CCA	GTG	CTG	CCC	ACT	GAC	AGC	GCC	2080
S	R	G	G	V	A	V	V	P	A	S	G	N	S	A	Q	G	S	T	A	656
AGC	CGA	GGT	GGA	GTG	GCC	GTG	GTC	CCC	GCA	TCA	GGT	AAT	TCT	GCC	CAA	GGC	TCA	ACT	GCC	2140
L	S	I	L	L	L	F	F	P	L	Q	L	W	V	T	*					672
CTC	TCT	ATC	CTA	CTC	CTT	TTC	TTC	CCC	CTG	CAG	CTC	TGG	GTC	ACC	TGA					2188
CCT	GTA	GCCTT	TAACCC	ACC	ATCAT	CCCA	AACTC	CTCCT	GTCTT	GCCTT	CATTCT	CTTAC	CCACCT	CTACCT	ATGGG					2267
TCT	CCA	ATCT	CGG	ATAT	CCACCT	TGT	GGGTAT	CTC	CAGCT	CTCC	GGTCTTT	TACCC	TGTGAT	CCCC	AGCCCC	GGCC	ACTGAC			2346
CAT	CTGT	GACCC	TTCC	CTGCC	ATTGG	GGCCCT	CCACCT	GTGGCT	CACAT	CTCG	CCAG	CCCC	CACAG	AGCAT	CCTC	AGGCCT				2425
CT	CAAG	GGTCC	TCAT	CACCT	ATTGC	AGCCTT	CAGGG	CTCGG	CTATTT	TCCACT	ACTCC	CTTTCAT	CCGCC	TGTGT	GCC					2504
GT	CCCC	TTTAG	CTGCC	TCCTAT	TGAT	CTC	AGGGA	AGCCT	TGGAG	TCCC	TTCTC	ACCCCT	CAACCT	CCGG	AGTCC	AGGAG				2583
A	ACCC	GTAC	CCCC	ACAG	AGCCTT	AAG	CAACT	ACTT	CTGT	GAA	GTATTT	TTTG	ACTG	TTT	CATG	GAAA	CAAG	CCCTT	GGA	2662
A	ATAA	ATCT	CTAT	TAA	ACCG	CTTT	GTAA	CCAAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	2730

Fig. 24E

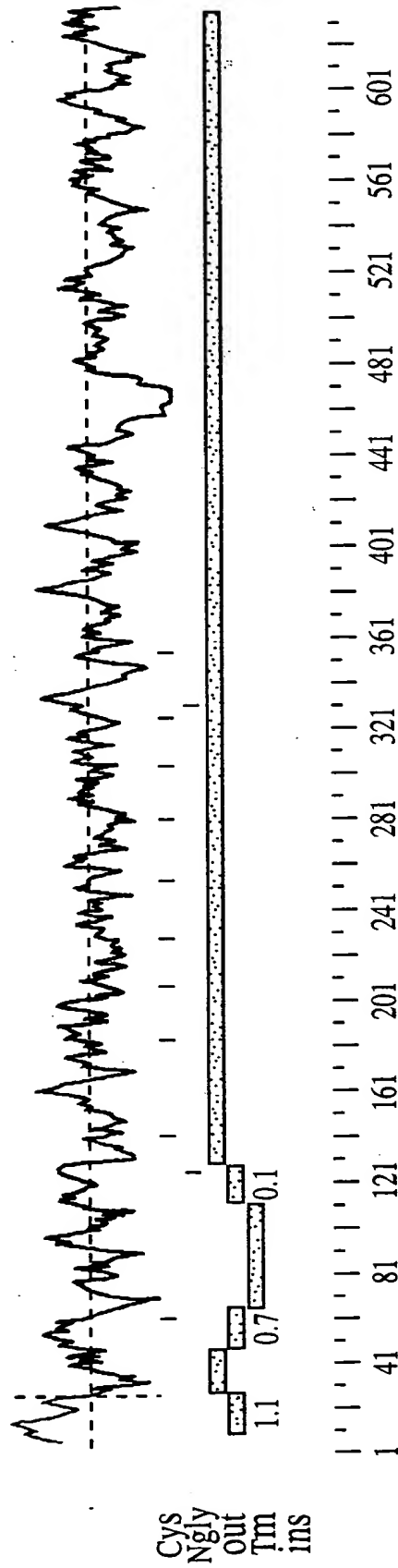


FIG. 24F

# LOCUS: GEF60

```

10      20      30      40      50      60      70
332 MAQLFLPLLAALVLAQAPALADVLEGDSSSEDRAFVRRIAGDAPLQGVLGALTIPCHVHYLRPPPSRRRA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF MAQLFLPLLAALVLAQAPALADVLEGDSSSEDRAFVRRIAGDAPLQGVLGALTIPCHVHYLRPPPSRRRA
10      20      30      40      50      60      70

80      90      100     110     120     130     140
332 VLGSPRVKWTFLSRGAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF VLGSPRVKWTFLSRGAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ
80      90      100     110     120     130     140

150     160     170     180     190     200     210
332 HGIDSSDAVEVKVGKGVVFLYREGSARYAFSFGAQACARIGAHIAATPEQLYAYLGGYEQCDAGWLS
      ::::::::::::::
BEF HGIDSSDAVE-----SS
150

220     230     240     250     260     270     280
332 QTVRYPIQTPREACYGMDMGFPGVNRNYGVVDDPDDLVDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQER
      : ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF Q--RYPIQTPREACYGMDMGFPGVNRNYGVVDDPDDLVDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQER
160     170     180     190     200     210     220

290     300     310     320     330     340     350
332 GAEIATTGQLYAAWDGGLDHCSPGWLADGSVRYPIVTPSQRCGGGLPGVKTLFLFPNQTFPNKHSRNFV
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF GAEIATTGQLYAAWDGGLDHCSPGWLADGSVRYPIVTPSQRCGGGLPGVKTLFLFPNQTFPNKHSRNFV
230     240     250     260     270     280     290

```

**Fig. 24G**

# 332 YCFRDSAQP-SAIPEASNPNASDGLAIVTVTETLLELQLPQEATESESRGAIYSIPIMEDGGGGSS

332 YCFRDSAQP-SAIPEASNPNASDGLAIVTVTETLLELQLPQEATESESRGAIYSIPIMEDGGGGSS  
 BEF YCFRDSAQLLPSLRPPTQPPTQL--DGLEAIVTVTETLLELQLPQEATESESRGAIYSIPIMEDGGGGSS  
 300 310 320 330 340 350

420 TPEDPAEAPRTLLEFETQSMVPPPTGFSEEEGKALEEEKYEDEEEKEEEEEVEDEALWAWPSELSSP  
 BEF TPEDPAEAPRTLLEFETQSMVPPPTGFSEEEGKALEEEKYEDEEEKEEEEEVEDEALWAWPSELSSP  
 360 370 380 390 400 410 420

490 GPEASLPTEPAAQKSLSQAPARAVLQPGASPLPDGESEASRPPRVHGPPTETLTPRERNLASPSPSTL  
 BEF GPEASLPTEPAAQEEESLSQAPARAVLQPGASPLPDGESEASRPPRVHGPPTETLTPRERNLASPSPSTL  
 430 440 450 460 470 480 490

560 VEAREVGEATGGPELSGVPRGESEETGSSEGAPSLLPATRAPEGTRELEAPSEDNSGRTAPAGTSVQQAQP  
 BEF VEAREVGEATGGPELSGVPRG-----GAR-----TQ-  
 500 510 520

630 VLPTDSASRGGVAVVPASGNSAQGSTALSILLFFFLQLWVT  
 BEF -----FAL-----  
 640 650 660 670

Fig. 24H

[illegible]

**Fig. 24I**





# Figure 24K

```

680      690      700      710      720      730      740
M GACYKHSTRRSWEAEQCRAALGAHLTISICTPEEQDFVNDRYEQWIGLNDRTIEGFLWSDGAPLLY
H -----SI-----L-----LLF
      660

750      760      770      780      790      800      810
M ENWNPQPDYSYFLSGENCVMVWHDQGWSDVPCNYHLSYCKMGLVSCGPPPLPLAQIFGRPRIRYAV
      :
H -----F-----PIQ-----
      670

820      830      840      850      860      870      880
M DTVLRYRCRDGLAQRNLPILRCQENGLWEAPQISCVPRRPGRALRSMDAPEGPRGQLSRHRKAPLTPPSS
      :
H -----LWVT-----
      670

```

M L

H -

**Fig. 24K**

```

10      20      30      40      50
H  GTCG-ACCCA-CG-----CGTCC-----GTCCTGGGCCCCAGCCTCTCTCCTCAGCTCGCGCAGTC
:: : ::::: :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GAGGCTCCCGGCGAGCTGGCGCCCTGTCTGGTCCCGCGCGCCCGGCC-CTGCTCGCGCCCGCGCA-TC
10      20      30      40      50      60

60      70      80      90      100     110     120
H  TCCGCCGAGTCTCAG-CTGCAGCTGCAGACTGAGCCGTGCACCCGGAGGAGACCCCCGGAGGAGGCCGA
: : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M  GC-GCCGCACTCTCGGTCTGCGGCTGCGGACGTGACGGCGGTGCGCGGAGGGGACCTC-----GCAA
70      80      90      100     110     120

130     140     150     160     170     180     190
H  CAAACTTCGCAGTGCCGCGACCCCAACCCAGCCCTGGGTAGCCTGCAGCATGGCCCAGCTGTTCTGCCCC
::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M  -GTTCTTC-----CATC-----AGTG---TGCAGAAATGATACCACCTGCTTCTGTCC
130     140     150     160     170

200     210     220     230     240     250     260
H  CTGCTGGCAGCCCTGGTCCTGGCCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAG
::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M  CTGCTGGCCGCTCTGGTCTGACCCCAAGCCCTTGCCTGCTGATGACCTGAAAGAAGACAGCTCGG
180     190     200     210     220     230     240

270     280     290     300     310     320     330
H  AGGACCGCGCTTTTCGCGTGCGCATCGGGGCGACCGCCACTGCAGGCGTGTCTCGCGCGGCCCTCAC
::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
M  AGGATCGAGCCCTCCGCGTGCGCATCG-GTGC--CGCGCAGCTGCGGGCGTGTGGGCGGTGCCCTGGC
250     260     270     280     290     300

```

Fig. 24L

**Fig. 24M**

[illegible]

**Fig. 24N**

	1040	1050	1060	1070	1080	1090	1100
H	GGCCAACTGTATGCAGCCTGGGATGGTGGCCTGGACCACTGCAGCCAGGGTGGCTAGCTGATGGCAGTG						
	1010	1020	1030	1040	1050	1060	1070
M	GGCCAGCTGTACGCAGCCTGGAAATGGTGGCCTGGACAGATGTAGCCCTGGCTGGCTGGCTGATGGCAGCG						
	1110	1120	1130	1140	1150	1160	1170
H	TGCGCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGGGGCTTGCCCTGGTGTCAAGACTCTCTTCCT						
	1080	1090	1100	1110	1120	1130	1140
M	TGCGCTATCCCATCATCACACCCAGCCAAACGCTGTGGGGCGGCTGCCAGGAGTCAAGACCCCTCTTCCT						
	1180	1190	1200	1210	1220	1230	1240
H	CTTCCCCAACCACTGGCTTCCCCCAATAAGCACAGCCGCTTCAACGCTCTACTGCTTCCGAGACTCGGGCC						
	1150	1160	1170	1180	1190	1200	1210
M	CTTTCCCCAACCACTGGCTTCCCCCAGCAAGCAGAACCGCTTCAATGTCTACTGCTTCCGAGACTCTGCCC						
	1250	1260	1270	1280	1290	1300	1310
H	CAGCCTTCTGCCATCCCCTGAGGCCTCCAACCCAGCCTCCAACCCAGCCTCTGTATGGACTAGAGGCTATCG						
	1220	1230	1240	1250	1260	1270	
M	CATCCCTCTGCTTCCCTCTGAGGCCTCTAGCCCAGCCTC-----AGATGGACTTGAGGCCATTG						
	1320	1330	1340	1350	1360	1370	1380
H	TCACAGTGACAGAGACCCCTGGAGGAACTGCAGCTGCCTCAGGAAGCCACAGAGAGTGAATCCCGTGGGGC						
	1280	1290	1300	1310	1320	1330	1340
M	TCACAGTGACAGAAAAGCTGGAGGAACTGCAGCTGCCTCAGGAAGCGATGGAGAGCGAGTCTCGTGGGGC						

Fig. 240

[illegible]

**Fig. 24P**

```

1730      1740      1750      1760      1770      1780      1790
H CATCACCACCTTCCTGATGGAGAGTCAGAAGCTTCCAGGCCCTCCAAGGGTCCATGGACCACCTACTGAGAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CGTCACCTTCTCCTG-----GGCCTCCAAGGTTCCGTGGACCGCCTGCAGAGAC
1670      1680      1690      1700      1710

1800      1810      1820      1830      1840      1850      1860
H TCTGCCCACTCCAGGAGAGAACCTAGCATCCCATCACCTTCCACTCTGGTTGAGGCAAGAGAGGTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TTTGCTCCCCCGAGGAGTGGAGC-----GCCACATCTACT-CC----TGGT-GGGGCAAGAGAAGTA
1720      1730      1740      1750      1760      1770

1870      1880      1890      1900      1910      1920      1930
H GGGAGGCAACTGGTGCTGAGCTATCTGGGTCCCTCGAGGAGAGAGCGAGGACAGGAAGCTCC-
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGGGGAAACTGGAGCCCTGAGCTCTCTGGGTTCTCTCGA--GAGAGCGAGGAGGCAGGGAGCTCCA
1780      1790      1800      1810      1820      1830

1940      1950      1960      1970      1980      1990      2000
H -----GAGGGTGCCCCCTTCCCTGCTTCCAGCCACACGGGCCCTGAGGGTACCAGGGAGCTGGAGGCCCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GCTTGAGGATGGCCCTTCCCTACTTCCAGCTACATGGGCCCTGTGGGTCCCAGGGAGCTGGAGACCCC
1840      1850      1860      1870      1880      1890      1900

2010      2020      2030      2040      2050      2060      2070
H CTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGACCTCAGTGCAGGCCACGCCAGTGTGCCCACT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CTCAGAAGAGAAGTCTGGAAGAACTGTCTCTGGCAGGCACCTCAGTGCAGGCCACGCCAGTGTGTGCCCAAC
1910      1920      1930      1940      1950      1960      1970

```

**Fig. 24Q**

```

2080      2090      2100      2110      2120      2130
H  GACAGCGCCAGCGAGGTGGAGTGGCCGTGGTCCCGCATCAGGTAATT-----CTGCCCAAGGCTCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GACAGTGCCAGCCACGGTGGAGTGGCTGTGGCTCCCTCATCAGGTGACTGTATCCCGAGCCCTGCCACA
1980      1990      2000      2010      2020      2030      2040
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  A-----C-TGC-----CCTCT--CTAT-----CCTA-CT-----CCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  ATGGTGGGACATGCTTGGAGGAGAAGGAGGTTTCCGCTGCCATGTTGCCAGGCTATGGGGGGGACCT
2050      2060      2070      2080      2090      2100      2110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2160      2170      2180      2190      2200
H  TTTC-----TTCCC--C---CTGCAGCTCTGG-----GTC--ACCTGA---CCTG---TAGTCCCTTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GTGCGATGTTGGCCTTCATTTCTGCAGCCCTGGCTGGGAGGCCCTTCCAGGGAGCCTGCTACAAGCACTTT
2120      2130      2140      2150      2160      2170      2180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2210      2220      2230
H  AACCCAC-----CA-----TCA-TCCCAAACTCT-----C---CTGTCC-----TTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  TCCACACGAAGGAGTTGGGAGGAGGCAGAAAGTCAGTGCCGAGCGCTAGGTGCTCATCTGACCAGCATCT
2190      2200      2210      2220      2230      2240      2250
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2240      2250      2260      2270
H  GC-----CT-----TCATTCTCT-TACCC---ACC---TCTACCTATGGGT---CTC-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GCACCCCTGAGGAGCAAGACTTTGTCAATGATCGATACCGGGAGTACCAGTGGATTTGGGCTCAATGACAG
2260      2270      2280      2290      2300      2310      2320

```

Fig. 24R



**Fig. 24S**

```

2490      2500      2510      2520      2530
H CTTCA-TCCGCCCTGTGTGCC-----GTCC---CCTTTAGCTGC-CTCCT-----ATTGATCTC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CCTCAGATTCTGTGTACCCCGGAGGCCCTGGCCGTGCTCTGCGCTCCATGGACGCCCCAGAACGACCAC
2680      2690      2700      2710      2720      2730      2740

2540      2550      2560      2570      2580
H AGGGA-AGC-----CTGGGAGTC-CC-TTCTCACC--CCTC-AACCTCCGGAGT-CCAGGAGAAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGGACAGCTCTCGAGGCACAGGAAGCACCGTTGACACCGCCCTCCAGTCTCTAGGGAGCCTGGAAGAC
2750      2760      2770      2780      2790      2800      2810

2590      2600      2610      2620      2630
H CCGTACCCCCCA-CAGAGCCTTAA-GCAACTACT-----TCT-----GTGAAGTATTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TGCTGCCCCCCAGCAGGACCCCTCTCACATCAACTGCCAGTGCTCTTCCCCATGATAGGGGTGACGTGAGA
2820      2830      2840      2850      2860      2870      2880

2640      2650
H ----TTTGACTGT--TTCA-----TGGAACA-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGGTGGGACTGAAATTTCAGAGGACAGCGCTCGAAGGGTTTCTGGGAACAACACTTGGTGGCTCCGCCCC
2890      2900      2910      2920      2930      2940      2950

2660      2670      2680
H -----AGCCTTGGAAT-----AAATCTCTATTAA-----AC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CTCACACAAGGCCCTCAGGTTTACCCGGTAAGTCCCTAAGTGCCTCAACTGCCCTCTCATGTCAGCTGC
2960      2970      2980      2990      3000      3010      3020

```

Fig. 24T

# Fig. 24U

```

      2690                                2700
H  CGCTTTGT-----AAC-----CAAAAAAAAAAAAAA
   : : : : :
M  CTCCTTGTCCCTCGATNCGTNAGGGACACTGTGCTATTGCTGATCTTGATTGTCGAAGAGTTTTTAGGAT
3030 3040 3050 3060 3070 3080 3090
      2710                                2720                                2730
H  AAA-----AAAAAAGGGCGG--CC-----GC
   : : : : :
M  GGAGTACCAGCAAAACCAGGTGGAAATAAAGTTGTCTGAACCCCAAGAAAAA
3100 3110 3120 3130 3140 3150

```

**Fig. 24U**

GTCGACCCACGGTCCGCCACCGCTCCGGCCC	ATG GCG CCG CCC GCC CGC CTC GCC CTG CTC	A A R L A L L	11
S A A A L T L A A R P A P S P G L G P G	31		
TCC GCC GCG GCG CTC ACG CTG GCG GCC CGG CCT AGC CCC GGC CTC GGC CCC GGA	126		
P E C F T A N G A D Y R G T Q N W T A L	51		
CCC GAG TGT TTC ACA GCC AAT GGT GCG GAT TAT AGG GGA ACA CAG AAC TGG ACA GCA CTA	186		
Q G G K P C L F W N E T F Q Q H P Y N T L	71		
CAA GGC GGG AAG CCA TGT CTG TTT TGG AAC GAG ACT TTC CAG CAT CCA TAC AAC ACT CTG	246		
K Y P N G E G G L G E H N Y C R N P D G	91		
AAA TAC CCC AAC GGG GAG GGG GGC CTG GGT GAG CAC AAC TAT TGC AGA AAT CCA GAT GGA	306		
D V S P W C Y V A E H E D G V Y W K Y C	111		
GAC GTG AGC CCC TGG TGC TAT GTG GCA GAG CAC GAG GAT GGT GTC TAC TGG AAG TAC TGT	366		
E I P A C Q M P G N L G C Y K D H G N P	131		
GAG ATA CCT GCT TGC CAG ATG CCT GGA AAC CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA	426		
P P L T G T S K T S N K L T I Q T C I S	151		
CCT CCT CTA ACT GGC ACC AGT AAA ACG TCC AAC AAA CTC ACC ATA CAA ACT TGC ATC AGT	486		
F C R S Q R F K F A G M E S G Y A C F C	171		
TTT TGT CGG AGT CAG AGG TTC AAG TTT GCT GGT ATG GAG TCA GGC TAT GCT TGC TTC TGT	546		

**Fig. 25A**

G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GGA	AAC	AAT	CCT	GAT	TAC	TGG	AAG	TAC	GGG	GAG	GCA	GCC	AGT	ACC	GAA	TGC	AAC	AGC	GTC	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
TGC	TTC	GGG	GAT	CAC	ACC	CAA	CCC	TGT	GGT	GGC	GAT	GGC	AGG	ATC	ATC	CTC	TTT	GAT	ACT	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	GCC	ATG	TCT	TCT	GTG	GTC	TAT	TCC	CCT	GAC	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
TTC	CCC	GAC	ACC	TAT	GCC	ACG	GGG	AGG	GTC	TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCG	GGG	GCC	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
TCC	CAC	ATC	CAC	TTC	AGC	TTC	CCC	CTA	TTT	GAC	ATC	AGG	GAC	TCG	GCG	GAC	ATG	GTG	GAG	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
CTT	CTG	GAT	GGC	TAC	ACC	CAC	CGT	GTC	CTA	GCC	CGC	TTC	CAC	GGG	AGG	AGC	CGC	CCA	CCT	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
CTG	TCC	TTC	AAC	GTC	TCT	CTG	GAC	TTC	GTC	ATC	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
CAG	GCC	CAG	GGA	TTT	GCT	GTT	TTA	TAC	CAA	GCC	GTC	AAG	GAA	GAA	CTG	CCA	CAG	GAG	AGG	1026

273/361

Fig. 25B

# TABLE 25C

P	A	V	N	Q	T	V	A	E	V	I	T	E	Q	A	N	L	S	V	S	351
CCC	GCT	GTC	AAC	CAG	ACG	GTG	GCC	GAG	GTG	ATC	ACG	GAG	CAG	GCC	AAC	CTC	AGT	GTC	AGC	1086
A	A	R	S	S	K	V	L	Y	V	I	T	T	S	P	S	H	P	P	Q	371
GCT	GCC	CGG	TCC	TCC	AAA	GTC	CTC	TAT	GTC	ATC	ACC	ACC	AGC	CCC	AGC	CAC	CCA	CCT	CAG	1146
T	V	P	G	S	N	S	W	A	P	P	M	G	A	G	S	H	R	V	E	391
ACT	GTC	CCA	GGT	AGC	AAT	TCC	TGG	GCG	CCA	CCC	ATG	GGG	GCT	GGA	AGC	CAC	AGA	GTT	GAA	1206
G	W	T	V	Y	G	L	A	T	L	L	I	L	T	V	T	A	I	V	A	411
GGA	TGG	ACA	GTC	TAT	GGT	CTG	GCA	ACT	CTC	CTC	ATC	CTC	ACA	GTC	ACA	GCC	ATT	GTA	GCA	1266
K	I	L	L	H	V	T	F	K	S	H	R	V	P	A	S	G	D	L	R	431
AAG	ATA	CTT	CTG	CAC	GTC	ACA	TTC	AAA	TCC	CAT	CGT	GTT	CCT	GCT	TCA	GGG	GAC	CTT	AGG	1326
D	C	H	Q	P	G	T	S	G	E	I	W	S	I	F	Y	K	P	S	T	451
GAT	TGT	CAT	CAA	CCA	GGG	ACT	TCG	GGG	GAA	ATC	TGG	AGC	ATT	TTT	TAC	AAG	CCT	TCC	ACT	1386
S	I	S	I	F	K	K	K	L	K	G	Q	S	Q	Q	D	D	R	N	P	471
TCA	ATT	TCC	ATC	TTT	AAG	AAG	AAA	CTC	AAG	GGT	CAG	AGT	CAA	CAA	GAT	GAC	CGC	AAT	CCC	1446
L	V	S	D	*																476
CTT	GTG	AGT	GAC	TAA																1461

Fig. 25C

AAACCCACTGTGCCCTAGGACTTGAGGTCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGTTCTTCTC 1540  
 TGACAGACTCTTCCCTCTCTCCCTCTGCCCTCGGCCTCTTTCGGGGAACCTCTCCTACAGACTAGGAAGAGGCACCT 1620  
 GGTGCCAGGGCAGGACAGCCTGGATTCTCTCTGCTT 1657

Fig. 25D

GTCGACCCACGGCTCCGCGCGGTCCCGGTGCTGCCCCCTCTGCCCCGGCGCGGGGTCCCGCACTGACGGCC 79  
 M A P A P A A R L A L L S A A A L T L A 19  
 C ATG GCG CCG CCC GCC GCC CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137  
 A R P A P A P G P R S G P E C F T A N G A D 39  
 GCC CGG CCC GCG CCC GGT CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197  
 Y R G T Q S W T A L Q G G K P C L F W N 59  
 TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC 257  
 E T F Q H P Y N T L K Y P N G E G L G 79  
 GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA GGA CTG GGC 317  
 E H N Y C R N P D G D V S P W C Y V A E 99  
 GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377

Fig. 25E

H	E	D	G	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N	119
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC	437	
L	G	C	Y	K	D	H	G	N	P	P	P	L	T	G	T	S	K	T	S	139	
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT	497	
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	F	K	F	A	159	
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT	557	
G	M	E	S	G	Y	A	C	F	C	G	N	N	P	D	Y	W	K	H	G	179	
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG	617	
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G	199	
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT	677	
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S	219	
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	737	
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V	239	
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC	797	
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F	259	
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT	857	
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L	279	
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG	917	

276/361

Fig. 25F



# FIG. 25G

V	R	L	S	G	R	S	R	P	P	L	S	F	N	V	S	L	D	F	V	299
GTC	CGG	CTC	AGT	GGG	AGG	AGC	CGC	CCG	CCT	CTG	TCT	TTC	AAT	GTC	TCT	CTG	GAT	TTT	GTC	977
I	L	Y	F	F	S	D	R	I	N	Q	A	Q	G	F	A	V	L	Y	Q	319
ATT	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	CAG	GCC	CAG	GGA	TTT	GCT	GTG	TTG	TAC	CAA	1037
A	T	K	E	E	P	P	Q	E	R	P	A	V	N	Q	T	L	A	E	V	339
GCC	ACC	AAG	GAG	GAA	CCG	CCA	CAG	GAG	AGA	CCT	GCT	GTC	AAC	CAG	ACC	CTG	GCA	GAG	GTG	1097
I	T	E	Q	A	N	L	S	V	S	A	A	H	S	S	K	V	L	Y	V	359
ATC	ACC	GAG	CAA	GCC	AAC	CTC	AGT	GTC	AGC	GCT	GCC	CAC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	1157
I	T	P	S	P	S	H	P	P	Q	T	A	Q	V	A	I	P	G	H	R	379
ATC	ACC	CCC	AGC	CCC	AGC	CAC	CCT	CCG	CAG	ACT	GCC	CAG	GTA	GCC	ATT	CCT	GGG	CAC	CGT	1217
Q	L	G	P	T	A	T	E	W	K	D	G	L	C	T	A	W	R	P	S	399
CAG	TTG	GGG	CCA	ACA	GCC	ACA	GAG	TGG	AAG	GAT	GGA	CTG	TGT	ACG	GCC	TGG	CGA	CCC	TCC	1277
S	S	S	Q	S	Q	Q	L	S	Q	R	F	F	C	M	S	H	L	N	L	419
TCA	TCC	TCA	CAG	TCA	CAG	CAG	TTG	TCG	CAA	AGA	TTC	TTC	TGC	ATG	TCA	CAT	TTA	AAT	CTC	1337
I	E	S	L	H	Q	E	T	L	G	T	V	V	S	L	G	L	L	E	I	439
ATC	GAG	TCC	CTG	CAT	CAG	GAG	ACC	TTA	GGG	ACT	GTC	GTC	AGC	CTG	GGG	CTT	CTG	GAG	ATA	1397
S	G	P	F	S	M	N	L	P	L	Q	S	P	S	L	R	R	S	S	R	459
TCT	GGA	CCA	TTT	TCT	ATG	AAC	CTT	CCA	CTA	CAA	TCT	CCA	TCT	TTA	AGA	AGA	AGC	TCA	AGG	1457

Fig. 25G

V R V N K M T A I P S \* 471  
GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA 1493

GTGACTGAAGCCACGCCCTGCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCCCTGAGTTCTCCTCTGATGAGTTC 1572  
CCTGCCCTTCCCATTCACCAACCATCTCTTTTGGAGACACCCCTGCTTTAGAGGCAGCCCCAGCCTGGATCCTCCATCACAT 1651  
GTACCAGCCTGGCTCTGCTGGGATAGTGAAGACAGGCCCCAGGCTGACAGGACACAGCTGGACCTGACTCCAGAAGA 1730  
CTCTTGGGTGGGAGGTATAGTGTAGGATGAGTTTCTTCTGCTTCTTCTGTTTGTCCACATACAGATCGGTTTC 1809  
CCCTGTCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTCAAGTTTCTAGGCTGGCCTGGTTCCCACTAAGA 1888  
GTGGCAATTGGCGCCCTAGAGGCCCAAGGCCAGTGAGGCTTTCTGCTGCCAACTACCATGTGTCTATCT 1967  
AGTCCGAGGGGACTGAGAGCAGGGCCACACCATGTCATCTTTCTAGAGGGTTCTTTTAGTACCCACTGACCAATGG 2046  
GGCAAGCCTGAGGATTGGTCCATCTGTTGTCCATGGAACAGACACAGTGAACCTCCTGGATACTAGACTTAACCTAGCC 2125  
TAGCCCTCAAGTAGTTGCCAATCCTGTGGAATCAGAAATTCAGCCTGTCTTCTGTCCCTCAGCCCCAAGCCTGTAGCCTAG 2204  
AGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGC 2283  
TGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCACAGAGCTGG 2362  
GGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAACTCAGCGATCAAGAGCTTGCTTTGTATACATCG 2441  
GACCCCTAGGTTCTATCCACGACCTATCAGAAAGGTGGGAGAGAAAAGACTGCACCATAGCATGCGGCAGCATCTGTGG 2520  
TTCCTACGTGAGGTGTCATCATTTTAAAGCAGATCAAAACTACCGCGAGTTTGTCTCTTGTCTCTTATCATGGGAGC 2599  
AGAGTAGGAGTAAGGCTCTGGTCTTGCTCATTTGTCCCCAGACAGGAGGCAGGAAAGTCAAGGCTTGGAACTGGA 2678  
GATCCCTCCAGGAAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGGAGAGGAAGGCCATCCCCGACTGAGAAAGTC 2757  
CTGCAGTCTGGAAAGTGGCCTTTGTACGACGAGCTGTGCCCCTGAAAGGTAGACCTTGGTCACTCTCCTGCCAGCCCTTGA 2836  
GCCTCTGCTCTCCTGGGTACCCCTCCTGGAACACCATGCTAACCTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCTC 2915  
TCCTCTAGCTGCTCTCCAGGACTGTCTGGGCCATCTGGGGATCAGGAGAGGCAGGAGTACTGACGAGGCAG 2994  
TGACCTGAGCTGATGAGTCAACCAGAGGACACAGAGTCTACAGTGGGCTGGCTGCTGGCTCAGCTCCTATGGGAGGCC 3073  
TACAGGGGTACTAAGCTAGGGGTCTATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC 3152  
CACTACATAAGAAGACCACTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC 3231

Fig. 25H

CCTGAGACCAAGTTGAGTCACAGAGTGCCATGTGCGTAGTGCCATAAAGGATATGGTTCTTAACCAGGGAAGGCTC 3310  
 ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACCTCACCTGTCTCTTCCT 3389  
 ATCTCGGACACAGGAAGCAAGCCCCAGTGTGTGGCAGCTGCGGCTCAGCATTTGGTGTCCCCAGGAAGGCGGTGGATG 3468  
 TGCCACGCTCCTTTTGTGTGGCCTGGCACAGCCCCAACACTGCAGGGCCACCTTCTCTCTTGGGGGTAGGGACAC 3547  
 ATAAGGAAAACATAACCCACCTCCAACAACAGCAGAGGACAGTGGGAAGGAAGGCTGTAAATCACCCAGGCCAGACCTC 3626  
 CAGAAATGACAGGCACAGTCTGTTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCTTTGTGCTGGTAACACCCCTGCCCTG 3705  
 GAGCATAGGGGTAAGCCGAGGAGAGAGCAGCCCTCAGAGACATCAGCTAAAAACATAGTGCCCCATGTCCCTCCCT 3784  
 TCCGTGCACACTGCTTACAAAGCAGAGACAGAGTAGGAAGAGGTCTTCATCCTCTCCACATCAGCAAGGATAGGGCT 3863  
 GCGGCTGCCATAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3942  
 AAAGCTCTTGAAGATCAAAGCTCTGGCGGTACAGCTGTCTGGCCTGTGGGCCAGCCCCATGGGATGTGCCCTGGGCCAG 4021  
 GTGCCACCCACGGCTCACTGTCAATCCAGGAGGACCCACCTGATGCTCCTCATCATCCGCTGGCCTGACACTATCA 4100  
 GAGCTCGCGCGGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGATGGCTCCAGA 4179  
 CTCTGTCAGCCTCTGCAGGGGCCACACAAGTCTCCCGAGGCCAAGTCCACAAAGCTCCATGGTTCCCTGGCTCCTCCT 4258  
 GTGGAGTGCTCCTGTTGATGTCTGAGGTCTGCTTTGGGTACCGCCTGGGAACCTGCTAACCTCCGATTTGGTCCCTTGT 4337  
 GTCCTGTTTACTGCTCCTTCTACCTCCAGGTCACTTAGCTCTGGCTGCTGGGTGGGAGTGGGGATGCT 4416  
 GGCTGACCCCCACCTGGTCTGCCAACAGAACCTGGGGGCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495  
 AACTGGCCCCAGGCTGAGTGGGCAGAGCAAAACAAGTGGAAGGGATCTCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT 4574  
 AGATCCAGCGAGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAATCTCACCCCTCCAGCAG 4653  
 GGATATGACTTTGGACAACAAGGCTTTATTTGTAAATATGCTCTTAATATGCAACTTTGAGAAATAAGATAGAAACATCA 4732  
 TGTATTTTAAATATAAATGAAGTGTGACACACTGTATACAATTTAATATATATATTTTAGGATTTTGTATTAAAGAA 4811  
 AATGGAATGTGATGGTACTTAACTTTTACAAAAGAGAGAAAATGTTATTTTACTGTTTGAAGAAAATAAATATTCTCA 4890  
 TTGTTGTAGAAAAAATAAAAAAAGGGGCGCCG 4928

Fig. 25I

Hum.	MAPPAARLALLSAAALTLAARPA	SPGLPGPECFTANGADYRG	TQNW	TALQGGKPC	LFWN	ETFOHPYNT	
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	MAPPAARLALLSAAALTLAARPA	GPGR--SGPECFTANGADYRG	TQSW	TALQGGKPC	LFWN	ETFOHPYNT	
	10	20	30	40	50	60	70
Hum.	LKYPNGEGGLGEHNYCRNP	DGVS	PWCYVAEHEDGVYWKYCEI	PACQMPGNLGCYKDHGN	PPPLTG	TGTSKT	
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	LKYPNGEGGLGEHNYCRNP	DGVS	PWCYVAEHEDGVYWKYCEI	PACQMPGNLGCYKDHGN	PPPLTG	TGTSKT	
	70	80	90	100	110	120	130
Hum.	SNKLTIQTCISFCRSQRFK	FAGMESGYACFCGNNPDYWKYGEAA	STECNSVCFGDHTQPCGGD	GRIILFD			
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	SNKLTIQTCISFCRSQRFK	FAGMESGYACFCGNNPDYWKHGEAA	STECNSVCFGDHTQPCGGD	GRIILFD			
	140	150	160	170	180	190	200
Hum.	TLVGACGGNYSAMSSVVYSP	DFPD	TYATGRVCYWTIRVPGASHIHFS	FPLFDIRDSADMVELLDGY	THRV		
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	TLVGACGGNYSAMAAVVYSP	DFPD	TYATGRVCYWTIRVPGASRIHF	NFTLEDIRDSADMVELLDGY	THRV		
	210	220	230	240	250	260	270

**Fig. 25J**

Hum.	290	300	310	320	330	340	350
	LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQAVKEELPQERPAPVNQTVAEVITEQANLSV						
	...	...	...	...	...	...	...
Mur.	280	290	300	310	320	330	340
	LVRLSGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQATKEEPPQERPAPVNQTVAEVITEQANLSV						
Hum.	360	370	380	390	400	410	420
	SAARSSKVLVYITTSPPSHPPQTVPGSNSWAPPMGAGSHRVEGWTVVYGLATLLILTVTAIVAKILLHVTFK						
	...	...	...	...	...	...	...
Mur.	350	360	370	380	390	400	410
	SAAHSSKVLVYITTSPPSHPPQTAQVAIPGHRQLGPTA---TEWKD-GLCTAWRPSSSSQSQQLSQRFFCM						
Hum.	430	440	450	460	470		
	SHRVPASGDLRDCHQPGTSGEISIFYKPSSTISIFKKKLKGSQ-QDDRNPLVSD						
	...	...	...	...	...	...	...
Mur.	420	430	440	450	460	470	
	SHLNLIESLHQETLGTVVVSLGLLEISGPFMSNPLQSPSLRRSSRVNVNKMTPAIPS						

Fig. 25K

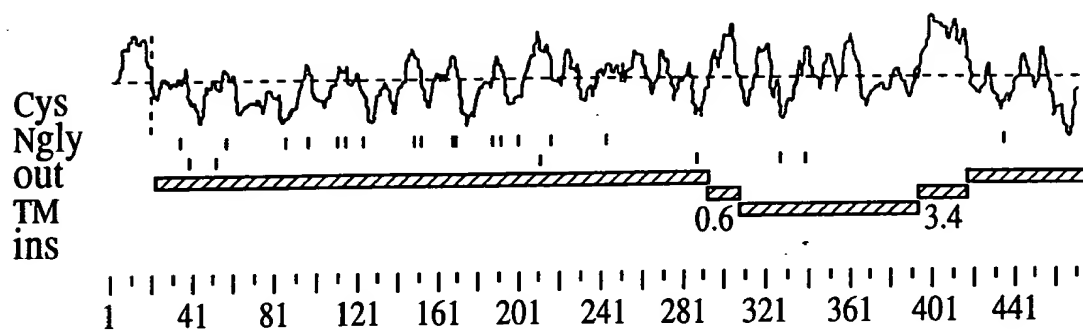


Fig. 25L

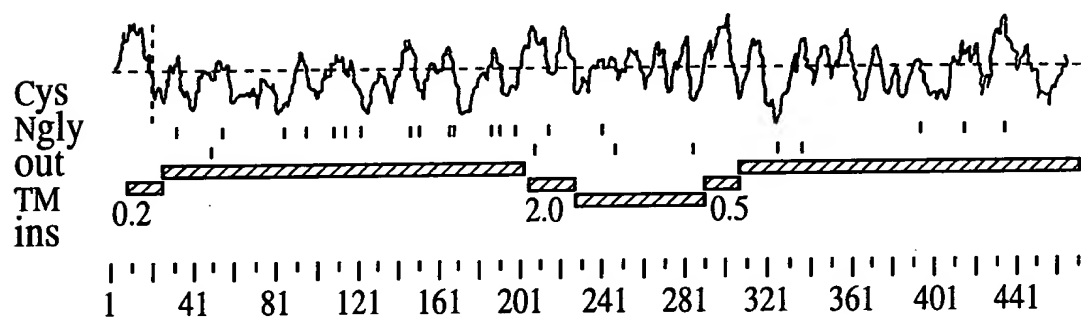


Fig. 25M

M M L P Q N S W H I D F G																13
GCGGCCGCTCGGATCTAGAACTAGTA ATG ATG CTG CCT CAA AAC TCG TGG CAT ATT GAT TTT GGA																66
R C C C H Q N L F S A V T C I L L N																33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GGT GTA ACT TGC ATC CTG CTC CTG AAT																126
S C F L I S S F N G T D L E L R L V N G																53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA																186
D G P C S G T V E V K F Q G Q W G T V C																73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT																246
D D G W N T T A S T V V C K Q L G C P F																93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT																306
S F A M F R F G Q A V T R H G K I W L D																113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT																366
D V S C Y G N E S A L W E C Q H R E W G																133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC TGC TGG GAA TGT CAA CAC CGG GAA TGG GGA																426
S H N C Y H G E D V G V N C Y G E A N L																153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT GGT GAA GCC AAT CTG																486

283/361

Fig. 26A

# Sequence

G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q	173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA	546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C	193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC	606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V	213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA	666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N	233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT	726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T	253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT	786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G	273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG	846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N	293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT	906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G	313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTT	GCT	GGC	966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G	333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT	1026

284/361

Fig. 26B



N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	T	I	393	
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

285/361

Fig. 26C

C	K	Q	L	G	C	G	K	P	M	H	V	F	G	M	T	Y	F	K	E	533
TGT	AAA	CAA	TTG	GGA	TGT	GGA	AAG	CCT	ATG	CAT	GTG	TTT	GGT	ATG	ACC	TAT	TTT	AAA	GAA	1626
A	S	G	P	I	W	L	D	D	V	S	C	I	G	N	E	S	N	I	W	553
GCA	TCA	GGA	CCT	ATT	TGG	CTG	GAT	GAC	GTT	TCT	TGC	ATT	GGA	AAT	GAG	TCA	AAT	ATC	TGG	1686
D	C	E	H	S	G	W	G	K	H	N	C	V	H	R	E	D	V	I	V	573
GAC	TGT	GAA	CAC	AGT	GGA	TGG	GGA	AAG	CAT	AAT	TGT	GTA	CAC	AGA	GAG	GAT	GTG	ATT	GTA	1746
T	C	S	G	D	A	T	W	G	L	R	L	V	G	G	S	N	R	C	S	593
ACC	TGC	TCA	GGT	GAT	GCA	ACA	TGG	GGC	CTG	AGG	CTG	GTG	GGC	GGC	AGC	AAC	CGC	TGC	TCG	1806
G	R	L	E	V	Y	F	Q	G	R	W	G	T	V	C	D	D	G	W	N	613
GGA	AGA	CTG	GAG	GTG	TAC	TTT	CAA	GGA	CGG	TGG	GGC	ACA	GTG	TGT	GAT	GAC	GGC	TGG	AAC	1866
S	K	A	A	A	V	V	C	S	Q	L	D	C	P	S	S	I	I	G	M	633
AGT	AAA	GCT	GCA	GCT	GTG	GTG	TGT	AGC	CAG	CTG	GAC	TGC	CCA	TCT	TCT	ATC	ATT	GGC	ATG	1926
G	L	G	N	A	S	T	G	Y	G	K	I	W	L	D	D	V	S	C	D	653
GGT	CTG	GGA	AAC	GCT	TCT	ACA	GGA	TAT	GGA	AAA	ATT	TGG	CTC	GAT	GAT	GTT	TCC	TGT	GAT	1986
G	D	E	S	D	L	W	S	C	R	N	S	G	W	G	N	N	D	C	S	673
GGA	GAT	GAG	TCA	GAT	CTC	TGG	TCA	TGC	AGG	AAC	AGT	GGG	TGG	GGA	AAT	AAT	GAC	TGC	AGT	2046
H	S	E	D	V	G	V	I	C	S	D	A	S	D	M	E	L	R	L	V	693
CAC	AGT	GAA	GAT	GTT	GGA	GTG	ATC	TGT	TCT	GAT	GCA	TCG	GAT	ATG	GAG	CTG	AGG	CTT	GTG	2106

**Fig. 26D**

G G S S R C A G K V E V N V Q G A V G I 713  
 GGT GGA AGC AGC AGG TGT GCT GGA AAA GTT GAG GTG AAT GTC CAG GGT GCC GTG GGA ATT 2166  
  
 L C A N G W G M N I A E V V C R Q L E C 733  
 CTG TGT GCT AAT GGC TGG GGA ATG AAC ATT GCT GAA GTT GTT TGC AGG CAA CTT GAA TGT 2226  
  
 G S A I R R V S R E P H F T E R T L H I L 753  
 GGG TCT GCA ATC AGG GTC TCC AGA GAG CCT CAT TTC ACA GAA AGA ACA TTA CAC ATC TTA 2286  
  
 M S N S G G C T G G E A S L W D C I R W E 773  
 ATG TCG AAT TCT GGC TGC ACT GGA GGG GAA GCC TCT CTC TGG GAT TGT ATA CGA TGG GAG 2346  
  
 W K Q T A C H L N M E A S L I C S A H R 793  
 TGG AAA CAG ACT GCG TGT CAT TTA AAT ATG GAA GCA AGT TTG ATC TGC TCA GCC CAC AGG 2406  
  
 Q P R L V G A D M P C S G R V E V K H A 813  
 CAG CCC AGG CTG GTT GGA GCT GAT ATG CCC TGC TCT GGA CGT GTT GAA GTG AAA CAT GCA 2466  
  
 D T W R S V C D S D F S L H A A N V L C 833  
 GAC ACA TGG CGC TCT GTC TGT GAT TCT TCT TTC TCT TCT CAT GCT GCC AAT GTG CTG TGC 2526  
  
 R E L N C G D A I S L S V G D H F G K G 853  
 AGA GAA TTA AAT TGT GGA GAT GCC ATA TCT CTT TCT TCT GTG GGA GAT CAC TTT GGA AAA GGG 2586  
  
 N G L T W A E K F Q C E G S E T H L A L 873  
 AAT GGT CTA ACT TGG GCC GAA AAG TTC CAG TGT GAA GGG AGT GAA ACT CAC CTT GCA TTA 2646

287/361

**Fig. 26E**

C	P	I	V	Q	H	P	E	D	T	C	I	H	S	R	E	V	G	V	V	893
TGC	CCC	ATT	GTT	CAA	CAT	CCG	GAA	GAC	ACT	TGT	ATC	CAC	AGC	AGA	GAA	GTT	GGA	GTT	GTC	2706
C	S	R	Y	T	D	V	R	L	V	N	G	K	S	Q	C	D	G	Q	V	913
TGT	TCC	CGA	TAT	ACA	GAT	GTC	CGA	CTT	GTG	AAT	GGC	AAA	TCC	CAG	TGT	GAC	GGG	CAA	GTG	2766
E	I	N	V	L	G	H	W	G	S	L	C	D	T	H	W	D	P	E	D	933
GAG	ATC	AAC	GTG	CTT	GGA	CAC	TGG	GGC	TCA	CTG	TGT	GAC	ACC	CAC	TGG	GAC	CCA	GAA	GAT	2826
A	R	V	L	C	R	Q	L	S	C	G	T	A	L	S	T	T	G	G	K	953
GCC	CGT	GTT	CTA	TGC	AGA	CAG	CTC	AGC	TGT	GGG	ACT	GCT	CTC	TCA	ACC	ACA	GGA	GGA	AAA	2886
Y	I	G	E	R	S	V	R	V	W	G	H	R	F	H	C	L	G	N	E	973
TAT	ATT	GGA	GAA	AGA	AGT	GTT	CGT	GTG	TGG	GGA	CAC	AGG	TTT	CAT	TGC	TTA	GGG	AAT	GAG	2946
S	L	L	D	N	C	Q	M	T	V	L	G	A	P	P	C	I	H	G	N	993
TCA	CTT	CTG	GAT	AAC	TGT	CAA	ATG	ACA	GTT	CTT	GGA	GCA	CCT	CCC	TGT	ATC	CAT	GGA	AAT	3006
T	V	S	V	I	C	T	G	S	L	T	Q	P	L	F	P	C	L	A	N	1013
ACT	GTC	TCT	GTG	ATC	TGC	ACA	GGA	AGC	CTG	ACC	CAG	CCA	CTG	TTT	CCA	TGC	CTC	GCA	AAT	3066
V	S	D	P	Y	L	S	A	V	P	E	G	S	A	L	I	C	L	E	D	1033
GTA	TCT	GAC	CCA	TAT	TTG	TCT	GCA	GTT	CCA	GAG	GGC	AGT	GCT	TTG	ATC	TGC	TTA	GAG	GAC	3126
K	R	L	R	L	V	D	G	D	S	R	C	A	G	R	V	E	I	Y	H	1053
AAA	CGG	CTC	CGC	CTA	GTG	GAT	GGG	GAC	AGC	CGC	TGT	GCC	GGG	AGA	GTA	GAG	ATC	TAT	CAC	3186

288/361

Fig. 26F

D G F W G T I C D D G G W D L S D A H V V 1073  
 GAC GGC TTC TGG GGC ACC ATC TGT GAT GAC GGC TGG GAC CTG AGC GAT GCC CAC GTG GTG 3246  
  
 C Q K L G C G V A F N A T V S A H F G E 1093  
 TGT CAA AAG CTG GGC TGT GGA GTG GCC TTC AAT GCC ACG GTC TCT GCT CAC TTT GGG GAG 3306  
  
 G S G P I W L D D L N C T G T E S H L W 1113  
 GGG TCA GGG CCC ATC TGG CTG GAT GAC CTG AAC TGC ACA GGA ACG GAG TCC CAC TTG TGG 3366  
  
 Q C P S R G W G Q H D C R H K E D A G V 1133  
 CAG TGC CCT TCC CGC GGC TGG GGC CAG CAC GAC TGC AGG CAC AAG GAG GAC GCA GGG GTC 3426  
  
 I C S E F T A L R L Y S E T E S C A 1153  
 ATC TGC TCA GAA TTC ACA GCC TTG AGG CTC TAC AGT GAA ACT GAA ACA GAG AGC TGT GCT 3486  
  
 G R L E V F Y N G T W G S V G R R N I T 1173  
 GGG AGA TTG GAA GTC TTC TAT AAC GGG ACC TGG GGC AGC GTC GGC AGG AAC ATC ACC 3546  
  
 T A I A G I V C R Q L G C G E N G V S 1193  
 ACA GCC ATA GCA GGC ATT GTG TGC AGG CAG CTG GGC TGT GGG GAG AAT GGA GTT GTC AGC 3606  
  
 L A P L S K T G S G F M W V D I Q C P 1213  
 CTC GCC CCT TTA TCT AAG ACA GGC TCT GGT TTC ATG TGG GTG GAT GAC ATT CAG TGT CCT 3666  
  
 K T H I S I W Q C L S A P W E R R I S S 1233  
 AAA ACG CAT ATC TCC ATA TGG CAG TGC CTG TCT GCC CCA TGG GAG CGA AGA ATC TCC AGC 3726

Fig. 26G

P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266

Fig. 26H



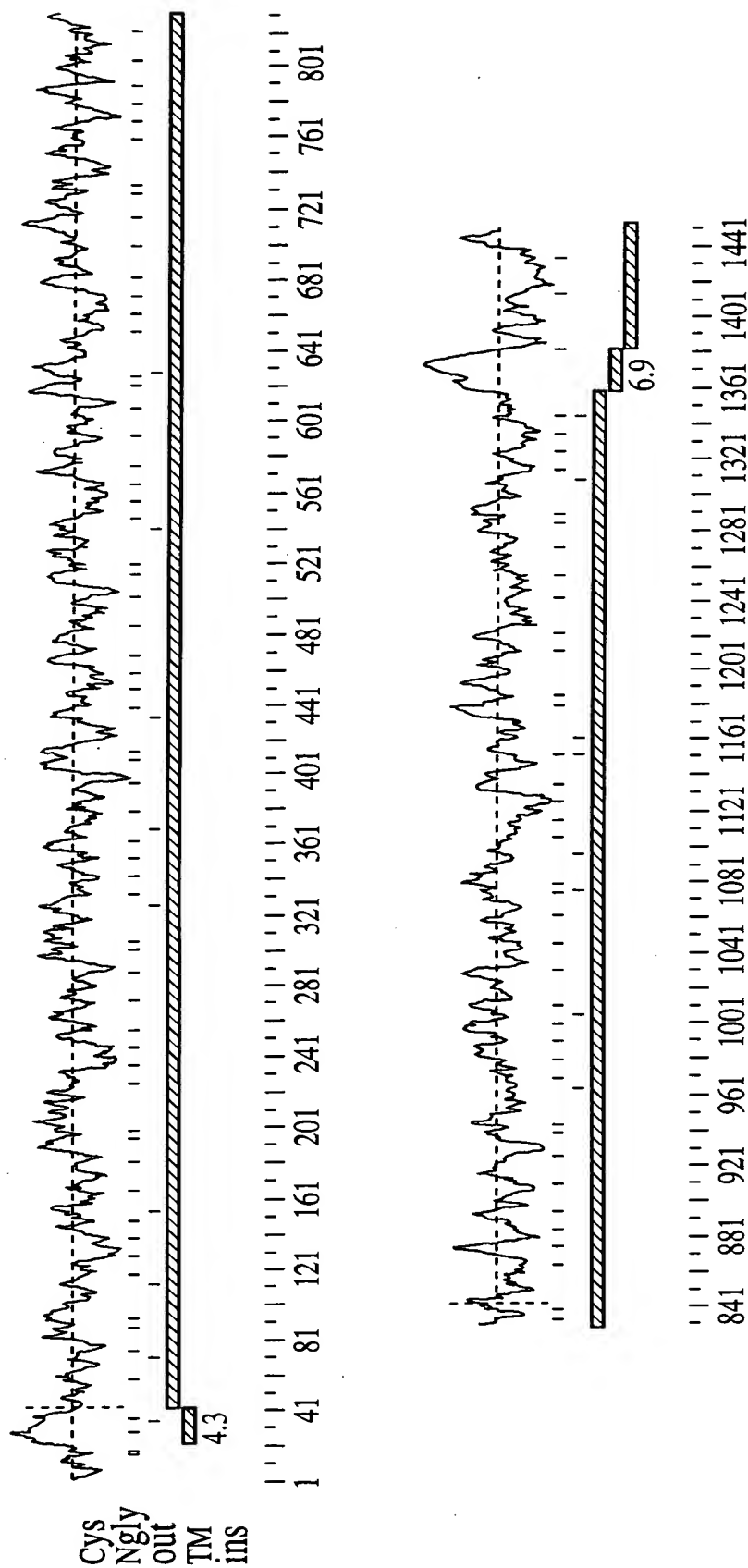


Fig. 26J



**Fig. 26K**

```

Hum. LKIQGRWGTVCHHKWNNAADVCKQLGCGTALHFAGLPHLQSGSDVWLDGVSCSGNESFLWDCRHSGET
    280 290 300 310 320 330 340
    .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 MNISQWRALCASHWLANANVICRQLGCGVAISTPGGPHLVEEGDQILTARFHCSGAESFLWSCPVTAL
    260 270 280 290 300 310 320

Hum. VNFDCLHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVCKQLGCPFSV
    350 360 370 380 390 400 410
    . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GGPDCSHGNTASVICS-GNQI-----QVLPQCND-----SV
    330 340 350

Hum. FGSRRAKPSNEARDIWINISICTGNESALWDCTYDGKAKRTCRRSDAGVICSDKADLRLVGAHSPCY
    420 430 440 450 460 470 480
    .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 -----SQPTGSA-----ASEDSA---PY-----CSDSRQL--RLVDGGGPACA
    360 370 380

Hum. GRLEVKYQGEWGTVCHDRWSTRNAADVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE
    490 500 510 520 530 540 550
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GRVEILDQGSWGTCDDGWDLDDARVVCRLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP
    390 400 410 420 430 440 450

```

**Fig. 26L**

Hum.	560	570	580	590	600	610	620
	HS	GW	GN	CV	H	R	E
	D	V	I	V	T	C	S
	G	D	A	T	W	G	L
	R	L	V	G	S	N	R
	C	S	G	R	L	E	V
	F	Y	F	Q	G	R	W
	T	V	C	D	D	G	W
	N	S	K	A	A	A	V
	V	C	S	Q	L	D	C
WC1	460	470	480	490	500	510	520
	S	R	G	W	Q	H	N
	C	R	H	K	Q	D	A
	G	V	I	C	S	--	E
	F	L	A	R	M	V	S
	E	D	Q	Q	C	A	G
	W	L	E	V	F	Y	N
	G	T	W	G	S	V	C
	R	N	P	M	E	D	I
	T	V	S	T	I	C	R
	Q	L	G	C			
Hum.	630	640	650	660	670	680	690
	P	S	I	I	G	M	G
	L	N	A	S	T	G	Y
	K	I	W	L	D	V	S
	C	D	E	S	D	L	W
	S	C	R	N	S	G	W
	G	N	D	C	S	H	E
	D	V	G	I	C	S	D
	A	S	D	M	E	L	R
	L	V	G	S			
WC1	530	540	550	560	570	580	590
	G	D	S	G	T	L	N
	S	S	V	A	L	R	E
	G	F	R	P	Q	W	D
	R	I	Q	C	R	K	T
	D	T	S	L	W	Q	C
	P	S	D	P	W	N	Y
	N	S	C	S	P	K	E
	E	A	I	W	C	A	D
	S	R	--	Q	I	R	L
	V	D	G	G			
Hum.	700	710	720	730	740	750	760
	S	R	C	A	G	K	V
	E	V	N	V	Q	A	V
	G	I	L	C	A	N	G
	M	N	I	A	E	V	V
	C	R	L	E	C	S	A
	I	R	S	R	E	P	H
	F	T	E	R	T	L	H
	I	L	M	S	N	S	G
	T	G	E	A	S	L	
WC1	600	610	620	630	640	650	660
	G	R	C	S	G	R	V
	E	I	L	D	Q	G	S
	W	G	T	I	C	D	R
	W	D	L	D	A	R	V
	V	C	K	Q	L	G	C
	E	A	L	D	A	T	V
	S	S	F	F	G	T	G
	S	G	P	I	W	L	D
	E	V	N	C	R	G	E
	E	S	Q	V			
Hum.	770	780	790	800	810	820	830
	W	D	C	I	R	W	E
	K	Q	T	A	C	H	L
	N	M	E	A	S	L	I
	C	S	A	H	R	Q	P
	R	L	V	G	A	D	M
	P	C	S	G	R	V	E
	K	H	A	D	T	W	R
	S	V	C	D	S	D	F
	S	L	H	A	A	N	V
	L	C	R	E	L		
WC1	670	680	690	700	710	720	730
	W	R	C	P	S	W	G
	R	Q	H	N	C	N	H
	Q	E	D	A	G	V	I
	C	S	G	F	--	V	R
	L	A	G	D	G	P	C
	S	G	R	V	E	H	S
	G	E	A	W	T	P	V
	S	D	G	N	F	T	L
	P	T	A	Q	V	I	C
	A	E	L				

Fig. 26M

840	850	860	870	880	890	900
Hum.	NCGDAISLSVGDHFGKGNGLTWA	KFCQCEGSETHLALCPIVQHP	EDTCIHSREVGVC	SRYT	DVRLV-NG	
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	GCGKAVSVLGHMPFRES	DGQVWAEFRCDGGEPELWSC	PRVPCPGGTC	LHSGAAQVVC	SVYTEVQLMKNG	
	740	750	760	770	780	790
						800
910	920	930	940	950	960	970
Hum.	KSQCDGQVEINVLGHWSL	CDTHWDPEDARVLCRQLSCGTAL	STTGKYGIGERSV	RWVGH	RHFC	CLGNESL
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	TSQCEGQVEMKISGRWRAL	CASHWSLANANVVC	RQLGCGVAISTPR	GPLHVEGGDQ	ISTAQFHC	SGAESF
	810	820	830	840	850	860
						870
980	990	1000	1010	1020	1030	1040
Hum.	LDNCQMTVLGAPPCIHGNT	VSIVICTGSLTQPLFPCLAN	VS	DPYLSAVPEGSALIC	LEDKRLRL	VDGDSRC
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	LWSCPVTALGGPDCSHGNT	ASVICSGNHTQVLPQCND	FLSQPAGSAA	SEESSPYCSD	SRQLRL	VDGGGPC
	880	890	900	910	920	930
						940
1050	1060	1070	1080	1090	1100	1110
Hum.	AGRVEIYHDGFWGTICDD	GWDLSDAHVVCQKL	CGVAFNATVSAHF	GEGSGPIW	LD	DLNCTG
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	GGRVEILDQGSWGTICDD	DDARVVC	RQLGCGEALNATG	SAHFAGSGPIW	LD	DLNCTG
	950	960	970	980	990	1000
						1010

Fig. 26N

**Fig. 260**

# Fig. 26P

```

1370      1380      1390      1400      1410
Hum.  LSSIFGLLLVLFILFTWCRVQK-----QKHLPLRVS-----TRRRG-----SLEENLFHEME
      :... :...: . : : :... . : : : :... :
WC1  LGSLLFLVLVILVTQLLRW-RAERRALSSYEDALAEAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAE
1290      1300      1310      1320      1330      1340      1350

      1420      1430      1440
Hum.  TC-----LKREDPHGTRTSD-----DTPNHGCEDAS-----DTSLLGV
      . : :...: . : : :... :
WC1  EVPVPGTSPSPSQNGNEEEVPPKEKGVRSSQTGSFLNFSREAAANPGEGEESFWLLQGKKGDAGYDDVELSA
1360      1370      1380      1390      1400      1410      1420

      1450
Hum.  LPASEAT-K
      : : :
WC1  LGTSPVTFS
1430

```

Fig. 26P

Hum.	ATGATGCTGCCCTCAAAACTCGTGGCATATTGATTTTGGAAGATGCTGTGCATCAGAACCTTTTCTCTG	10	20
WC1	ATG-----GCTC-TGG-----GCAGACA-----CCTCT-CCCTG	10	20
Hum.	CTGTGGTAACTTGCATCCTGCTCCTGAAATTCCTGCTTTCTCATCAGCAGTTTAAATGGAACAGATTGGA	80	140
WC1	C-GGGGACTCT-GTGTCTCTCTCTCT-----CGGCA-----CATGTTGGTGTGTCAGCTCTGGA	30	80
Hum.	GTTGAGGCTGGTCAATGGAGACGGTCCCTGCTCTGGACAGTGGAGGTGAAATTCAGGGACAGTGGGG	150	210
WC1	GCTGAGGTTGAAGGATGGAGTCCATCGCTGTGAGGGGAGAGTGGAAGTGAAGCACCAAGGAGAAATGGGGC	90	150
Hum.	ACTGTGTGATGATGGGTGGAACACTACTGCCT-CAACTGTCGTGTGCAAAACAGCTTGGATGTCCATTT	220	270
WC1	ACAGTGGATGTTACAGGTGGA-CATTGAAGGATGCATCTGTAGTGTGCAGACAGCTGGGTGTGGAGCT	160	210

**Fig. 26Q-1**

**Fig. 26Q-2**



	560	570	580	590	600	610	620
Hum.	ACTTGAA TACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTTATTCTTCTGGAGTTGT						
	...	...	...	...	...	...	...
WC1	TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG						
	490	500		510		520	
	630	640	650	660	670	680	690
Hum.	TAATAGCCCTGCTGTATTGCGCCCATTTGGCTGGATGACATTTATGCCAGGGAATGAGTTGGCACT-						
	...	...	...	...	...	...	...
WC1	TTGTGGC-----AAGGCTG--TGTCTGT-----CCTGGGACATGAG-----CTCTT						
	530		540		550	560	
	700	710	720	730	740	750	760
Hum.	CTGGAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT						
	...	...	...	...	...	...	...
WC1	CAGAGAGTCCAGT-GCC-----CAGGTCTG--GGC-----TGAAGAGTTCA-----GG						
	570	580		590		600	
	770	780	790	800	810	820	830
Hum.	TATGATAGTAGTGATCTTGAACTAAGGCTTGTAGGTGGAACCTAACCGCTGTATGGGGAGAGTAGAGCTGA						
	...	...	...	...	...	...	...
WC1	TGTGAGGGGAGGAGCCTGAGCT---CT-----GGGTCTGCCC-CAGAGTG-----CCCTG-						
	610	620	630		640		650

Fig. 26Q-3

Figure 26Q-4

```

      840      850      860      870      880      890      900
Hum.  AAATCCAAGGAGGTGGGGACCGGTATGCCACCATAAGTGGAAACAATGCTGCAGCTGATGTCGTATGCAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ---TCCA-----GGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT
      660      670      680      690      700      710      720      730      740      750      760

      910      920      930      940      950      960      970
Hum.  GCAGTTGGGATGTGGAACCGCACTTCACCTCGCTGGCTTGCCCTCATTTCAGTCAGGGCTGATGTTGTA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ACT-----CAGAAAGTCCGGCTCATGACAA-AC-GGCT--CCCTC-TCAG-TGTGAAGGGCAGGTGGAGAT
      710      720      730      740      750      760

      980      990      1000      1010      1020      1030      1040
Hum.  TGGCTTGATGGTGTCTCCTGCTCCGGTAATGAATCTTTCTTTGGGACTGCAGACATTCCGGAACCGTCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GAACATT-----TCTG-GACAATGGAGAGCGCTCTGTGCCTCCC-CTGGAGTCTGGCCAATGCC---A
      770      780      790      800      810      820

      1050      1060      1070      1080      1090      1100      1110
Hum.  ATTTTGACTGTCTTCATCAAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTTGGAACCTGCGACT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ATGTTATCTGTCGTCAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT
      830      840      850      860      870      880

```

Fig. 26Q-4



	1400	1410	1420	1430	1440	1450	1460
Hum.	CTGGAGTAATTGTTCTGTATAAGGCAGATCTGGACCTAAGGCTTGTCGGGGCTCATAGCCCCCTGTTATGG						
	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::
WC1	CTCAGA-----CAG--CAGGCAGCTCCG--CCTGGTG---GACGGGG-GC--GGTCCCTGCGCCGG						
	1110	1120	1130	1140	1150	1160	
	1470	1480	1490	1500	1510	1520	
Hum.	GAGATTGGAGGTGAATAACCAAGGAGAGTGGGGGACTGTGTGTCATGACAGATGGAGCACAAAGG-AATGC						
	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::
WC1	GAGAGTGGAGATCCTTGACCAAGGGCTCCTGSGGCACCATCTGTGATGACGGCTGGGAC-CTGGACGATGC						
	1170	1180	1190	1200	1210	1220	
	1530	1540	1550	1560	1570	1580	1590
Hum.	A-GCTGTTGTGTAAACAATTTGGATGTGA-AAGCCTATGCAATGTGTTGGTATGACCTATTTTAAAG						
	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::
WC1	CCGC-GTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCA-ATGCCACGGGGTCTGCTCACTTCGGGG						
	1230	1240	1250	1260	1270	1280	1290
	1600	1610	1620	1630	1640	1650	1660
Hum.	AAGCATCAGGACCTATTGGCTGGATGACGTTTCTTGCAATGGAAATGAGTCAAATATCTGGGACTGTGA						
	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::
WC1	CAGGATCAGGGCCCATCTGGTTGGACAACCTGAAGTGCACAGGAAAGGAGTCCCACGTGTGGAGGTGCC						
	1300	1310	1320	1330	1340	1350	1360

Fig. 26Q-6

Figure 26Q-7

```

1670      1680      1690      1700      1710      1720      1730
Hum. ACACAGTGGATGGGAAAGCATAATTGTGTACACAGAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 TTCCCGGGGCTGGGGCAGCACAACTGCAGACACACAAGCAGGACGCGGGGTCACTGCTCAG--AGTTC-
1370      1380      1390      1400      1410      1420      1430

1740      1750      1760      1770      1780      1790      1800
Hum. ACATGGGGCCTGAGGCTGGTGGCGGCGCAGCAACCGCTGCTCGGGAAGACTGGAGGTGTACTTCAAGGAC
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 -CT--GCCCTCAGGATGGTGAGTGAGGACCAGCAGTGTGCTGGGTGGCTGGAAGTTTCTACAATGGGA
1440      1450      1460      1470      1480      1490      1500

1810      1820      1830      1840      1850      1860      1870
Hum. GGTGGGCACAGTGTGTGATGACGGCTGGAACAGTAAGCTGCAGCTGTGGTGTAGCCAGCTGGACTG
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 CCTGGGGCAGTGTCTGCCGTAACCCCATGGAAGACATCACTGTGTCCACGATCTGCAGACAGCTTGGCTG
1510      1520      1530      1540      1550      1560      1570

1880      1890      1900      1910      1920      1930      1940
Hum. CCCATCTTCTATCATTTGGCATGGGTCTG-GGAAACGCTTCTA-CAGGATATGAAAAAATTGGCTCGATG
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 T--GGGGACAGTGGAAACCCCTCAACTCTTCTGTGCTCTTAGAGAAGGTTTtagccCACAGTGGGTGGAT-
1580      1590      1600      1610      1620      1630

```

Fig. 26Q-7

	1950	1960	1970	1980	1990	2000	2010
Hum.	ATGTTTCC	TGATGG	AGATGAG	TCTCTG	TGTCATG	CAGGAAC	AGTGGTG--GGGAAATAATGAC
	.....	.....	.....	.....	.....	.....	.....
WC1	-AGAA	TCCAGT	GTCTGG	AAACTG	ACACCT	CTCTCT	--CTGGCAGTGTCCCTTCTGACCCCTTGGAATTACAAC
	1640	1650	1660	1670	1680	1690	1700
	2020	2030	2040	2050	2060	2070	2080
Hum.	TGCAGT	CACAGT	GAAAGAT	GTGGAG	TG-ATCT	GTCTGATG	-CATCGGATATGGAGCTGAGGCTGTGTGGG
	::	::	::	::	::	::	::
WC1	T-CAT	GCTCT	CCTCAA	AGGAGG	AGCC	TATATCT	GTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGA
	1710	1720	1730	1740	1750	1760	
	2090	2100	2110	2120	2130	2140	2150
Hum.	TGGAAG	CAGCAG	GTGTG	CTGGAA	AGTTG	AGGTGA	ATGTCCAGGGTCCCGTGGGAATTCGTGTGCTAAT
	::::	::	::	::	::	::	::
WC1	TGGAG	GTGGT	CGCTG	CTCTGG	GAGAGT	GGAGAT	CTCTGACCAAGGCTCCTGGGGCACCATCTGTGATGAC
	1770	1780	1790	1800	1810	1820	1830
	2160	2170	2180	2190	2200	2210	2220
Hum.	GGCTGG	GGAAT	GAACAT	TGCTGA	AGTTGT	TGCAGG	CAACTTGAATGTGGGTCTGCAATCAGGGTCTCCA
	::::	::::	::::	::::	::::	::::	::::
WC1	CGCTGG	GACCT	GGACG	ATGCC	CGTGT	GTGTG	CAAGCAGCTGGGCTGTGGAGAAGC--CCTGGACGCCA
	1840	1850	1860	1870	1880	1890	1900

Fig. 26Q-8

Figure 26Q-9

	2230	2240	2250	2260	2270	2280
Hum.	GAGA-GCCTCATTTACAGAA--AGAACATTACACATCTTAATGTCGAATCTGGCTGCACTGGAGGGGA					
	..	: : : :	..	: : : :	: : : :	: : : :
WC1	CTGTCTCTTCCCTTTCGGACGGGATCAGGGCCCATCTGGCTGGATGAAGTGAAGTGCAGAGAGAGGA	1910	1920	1930	1940	1950
	1910	1920	1930	1940	1950	1960
	1970					
	2290	2300	2310	2320	2330	2340
Hum.	AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAAACAG-ACTGCGTGTCAATTTAAATATGGAAGCAAG					
	. :	: : : :	: : : :	: : : :	: : : :	: : : :
WC1	GTCCCAAGTATGAGGTGCCCTTCCTGGGGATGGCGCAACACAAC-TGCAATCATCAAGAAGATGCAGG	1980	1990	2000	2010	2020
	1980	1990	2000	2010	2020	2030
	2040					
	2360	2370	2380	2390	2400	2410
Hum.	TTTGATCTGCTCAGCCACAGGCAGCCAGGCTGTTGGAGCTGATATGCCCTGCTCTGGACGTGTGAA					
	. :	: : : :	: : : :	: : : :	: : : :	: : : :
WC1	AGTCATCTGCTCAGGATTGTGC-----GTCTGGCTGGAGGAGATGGACCCCTGCTCAGGGCGAGTAGAA	2050	2060	2070	2080	2090
	2050	2060	2070	2080	2090	2100
	2430	2440	2450	2460	2470	2480
Hum.	GTGAACATGCAGACACATGGCGCTCTGTCTGTGATTCTGATTCTCTCTCTCATGCTGCCAATGT--GCT					
	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
WC1	GTGCATTCTGGAGAAAGCCTGGACCCAGTGTCTGTATGGAAACTTCACACTCCCCACTGCCAGGTCATCT	2110	2120	2130	2140	2150
	2110	2120	2130	2140	2150	2160
	2170					

Fig. 26Q-9

	2500	2510	2520	2530	2540	2550	2560
Hum.	GTGCAGAGAA	TAAATTGTGGAGATGCCATA	TCTTCTGTGGGAGATCACT	TTGGAAAAGGG	-AATGG		
	.....	.....	.....	.....	.....	.....	.....
WC1	GTGCAGAGC	-TGGGATGTGGCAAGGCTGTGTCT	-GTCCTGGGACACATGCCATT	CAGAGATCCGATGG			
	2180	2190	2200	2210	2220	2230	2240
	2570	2580	2590	2600	2610	2620	2630
Hum.	TCTAACTTGGGCCG	AAAAAGTTCCAGTGTGAAGGAGTGAA	ACTCACCTTGCA	TATGCCCCAT	TGTTCAA		
	....	.....	.....	.....	.....	.....	.....
WC1	CCAGGTCTGGGCTGAAGAGTT	CAGGTGTGATGGGGGGAGCCTGAGCTCTGGT	CCTGCCCCAGAGTGCCC				
	2250	2260	2270	2280	2290	2300	2310
	2640	2650	2660	2670	2680	2690	2700
Hum.	CATCCGGAAGACACT	TGTATCCACAGCAGAGAAGTTGGAGTTGTCTGT	TCCCGATATACAGATGTCCGAC				
	.....	.....	.....	.....	.....	.....	.....
WC1	TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGT	TCAGTGTACACAGAAGTCCAGC					
	2320	2330	2340	2350	2360	2370	2380
	2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATGGCAAATCC	--CAGTGTGACGGGCAAGTGGAGATCAACGTGCT	-TGGACACTGGGGCTCAC				
	.....	.....	.....	.....	.....	.....	.....
WC1	TTATGAAAAACGGCACCTCTCAATGTGAGGGGCAGGTGGAGAT	-GAAGATCTCTGGACGATGGAGAGCGC					
	2390	2400	2410	2420	2430	2440	2450

Fig. 26Q-10



**Fig. 26Q-11**

**Fig. 26Q-12**

...

•

**Fig. 26Q-13**

TCCTTGGG

```

3550      3560      3570      3580      3590      3600
Hum.  TGCAGGCAGCTGGGCTGTGGGAGAAATGGAGTTGTACGCCCTCGCCCCCTTA--TCT-AAGACAGGCTCTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  TGCAGACAGCTTGGATGTGGGGACAGTGGA--AGTCT-CAACACCTCTGTGTGGTCTCAGGGAAGGTTCTA
3220      3230      3240      3250      3260      3270      3280

3610      3620      3630      3640      3650      3660      3670
Hum.  GTTTCATGTGGGTGGATGACATTTCAGTGTCCCTAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GACCCCGGTGGTAGATTAAATTCAGTGTCCGGAAATGGATACCTCTCTCTGTCAGTGTCCCTCTCTGGCCC
3290      3300      3310      3320      3330      3340      3350

3680      3690      3700      3710      3720      3730      3740
Hum.  ATGGAGCCGAAGAAATCTCCAGCCCAGCAGAGACCTGGATCACATGTGAAGATAGAATA---AGAG-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ATGGAAATACAGTTCATGCTCTCCAAAGGAGGAAGCCTACATCTCATGTGAAGGAAGACCCCAAGAGC
3360      3370      3380      3390      3400      3410      3420

```

Fig. 26Q-14

**Fig. 26Q-15**

# TOP-GENE

```

3910      3920      3930      3940      3950      3960      3970
Hum.  GGAAC TGAAC CATCTGG TTGATGACATGCGGTGCAAGGAAATGAGTCATTCTATGGGACTGTCACG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GGAAATGGGAGCATCTGGCTGGACGAGGTGCAGTGGGGGGCCGGGAGTCCTCCCTGTGGGACTGTGTTG
3640      3650      3660      3670      3680      3690      3700

3980      3990      4000      4010      4020      4030      4040
Hum.  CCAAA CCGTGGGACAGAGTGA CTGTGGACACAAAGGAAGATGCTGGCGTGAGGTGCTCTGG--ACAGTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CGGAGCCCTGGGGCAGAGCGACTGCAAGCACGAGGAGGATGCTGGTGTGAGGTGCTCTGGTGTAAAGGAC
3710      3720      3730      3740      3750      3760      3770

4050      4060      4070      4080      4090
Hum.  G-----CTGAAATCACTGAATG--CCT-----CCTCAGGT-CATT---TAGCA-CTTATTTTATCCA
      : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   AACATTGCCCCACGACCACAGCAGGACCAGAACCAACCTCAAATTCTCTCCCTGGCATCTTCTCCCTGCCT
3780      3790      3800      3810      3820      3830      3840

```

**Fig. 26Q-16**

```

Hum.  G-----TATCTT-----TGGGCTC-CTTCTC-----CTGGTTCT-----GTTTATCTATTCTCA
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
WC1  GGGTTCTCTGCCCTTATCCTGGGGTCGCTTCTCTCCCTGGTCCTCGTCATCCTGGTGACTCAGCTACTCA
3850 3860 3870 3880 3890 3900 3910

Hum.  CGTGGTG--CCGAGTTCAGAAACAAAACATCT-----GCC--CT---CAGAGTT-----
      .:.:.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GATGGAGAGCAGAGCGCAGAGCCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT
3920 3930 3940 3950 3960 3970 3980

Hum.  -----CAAC-----CAGAAGGAGGG---GTTCT-CTCG---AGGAGAAATTATCCATGA-----
      :... : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CGATTACCTTCTGACACAGAAAGGAAGGTCTGGGCAGCCAGATCAGATGACTGATGTCCCTGATGAAAAAT
3990 4000 4010 4020 4030 4040 4050

```

Fig. 26Q-17

TCF7D: GEF65260

```

4230                                4240                                4250
Hum.  ---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC
      :::::      :::::      :::::      :::::      :::::
WC1  TATGATGATGCTGAAGAAAGTACCAGTGCCTGGAACCTCTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
4060      4070      4080      4090      4100      4110      4120

4260      4270      4280      4290
Hum.  CCACATGGGACAAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :::: ::::: ::::: ::::: :::::
WC1  CCCCAGAGAAGGAGGACGGGTGAGGTCCCTCTCAGACAGGCTCTTCCCTGAACCTCTCCAGAGAGGCAGC
4130      4140      4150      4160      4170      4180      4190

4300      4310      4320      4330
Hum.  ----CCATGGTT--GTGAAGA---TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . ::::: : ::::: ::::: .. ::::: .. :::::
WC1  TAATCCTGGGGAAGGAGAGAAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGGATGCTGGGTATGATGAT
4200      4210      4220      4230      4240      4250      4260

```

Fig. 26Q-18



4340 4350

Hum. CTT-----CCTG-----CCTCTGAAGCCACAAAA

Food Type	Number of People
Fruit	2
Vegetables	4
Grains	3
Protein	2
Dairy	2

WC1 GTTGAACTCAGTGCCCTGGGAACATCCCCAGTGACTTTCTCG

4270	4280	4290	4300
------	------	------	------

**Fig. 26Q-19**

GTCGACCCACGGTCCGGTCTGTGGCTGAGC	M	A	L	P	A	L	G	L	D	P	W	S	12
	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GAC	CCC	TGG	AGC	67
L L G L L F L F L L Q L L L P T T A G													32
CTC CTG GGC CTT TTC CTC TTC CAA CTG CTT CAG CTG CTG CCG ACG ACG ACC GCG GGG													127
G G G Q G P M P R V R Y Y A G D E R A													52
GGA GGC GGC CAG GGC CCC ATG CCC AGG GTC AGA TAC TAT GCA GGG GAT GAA CGT AGG GCA													187
L S F F H Q K G L Q D F D T L L L S G D													72
CTT AGC TTC TTC CAC CAG AAG GGC CTC CAG GAT TTT GAC ACT CTG CTC CTG AGT GGT GAT													247
G N T L L Y V G A R E A I L A L D I Q D P													92
GGA AAT ACT CTC TAC TAC GTG GGG GCT CGA GAA GCC ATT CTG GCC TTG GAT ATC CAG GAT CCA													307
G V P R L K N M I P W P A S D R K K S E													112
GGG GTC CCC AGG CTA AAG AAC ATG ATA CCG TGG CCA GCC AGT GAC AGA AAA AAG AGT GAA													367
C A F K K K S N E T Q C F N F I R V L V													132
TGT GCC TTT AAG AAG AAG AGC AAT GAG ACA CAG TGT TTC AAC TTC ATC CGT GTC CTG GTT													427
S Y N V T H L Y T C G T F A F S P A C T													152
TCT TAC AAT GTC ACC CAT CTC TAC ACC TGC GGC ACC TTC GCC TTC AGC CCT GCT TGT ACC													487
F I E L Q D S Y L L P I S E D K V M E G													172
TTC ATT GAA CTT CAA GAT TCC TAC CTG TTG CCC ATC TCG GAG GAC AAG GTC ATG GAG GGA													547

Fig. 27A

K G Q S P F D P A H K H T A V L V D G M 192  
 AAA GGC CAA AGC CCC TTT GAC CCC GCT CAC AAG CAT ACG GCT GTC TTG GTG GAT GGG ATG 607  
  
 L Y S G T M N N F L G S E P I L M R T L 212  
 CTC TAT TCT GGT ACT ATG AAC AAC TTC CTG GGC AGT GAG CCC ATC CTG ATG CGC ACA CTG 667  
  
 G S Q P V L K T D N F L R W L H H D A S 232  
 GGA TCC CAG CCT GTC CTC AAG ACC GAC AAC TTC CTC CGC TGG CTG CAT CAT GAC GCC TCC 727  
  
 F V A A I P S T Q V V Y F F E E T A S 252  
 TTT GTG GCA GCC ATC CCT TCG ACC CAG GTC GTC TAC TTC TTC TTC GAG GAG ACA GCC AGC 787  
  
 E F D F F E R L H T S R V A R V C K N D 272  
 GAG TTT GAC TTC TTT GAG AGG CTC CAC ACA TCG CGG GTG GCT AGA GTC TGC AAG AAT GAC 847  
  
 V G G E K L L Q K K W T T F L K A Q L L 292  
 GTG GGC GGC GAA AAG CTG CTG CAG AAG AAG TGG ACC ACC TTC CTG AAG GCC CAG CTG CTC 907  
  
 C T Q P G Q L P F N V I R H A V L L P A 312  
 TGC ACC CAG CCG GGC CAG CTG CCC TTC AAC GTC ATC CGC CAC GCG GTC CTG CTC CCC GCC 967  
  
 D S P T A P H I Y A V F T S Q W Q V G G 332  
 GAT TCT CCC ACA GCT CCC CAC ATC TAC GCA GTC TTC ACC TTC CAG TGG CAG GTT GGC GGG 1027  
  
 T R S S A V C A F S L L D I E R V F K G 352  
 ACC AGG AGC TCT GCG GTT TGT GCC TTC TCT CTC TTG GAC ATT GAA CGT GTC TTT AAG GGC 1087

Fig. 27B

TABLE 27C

K	Y	K	E	L	N	K	E	T	S	R	W	T	T	Y	R	G	P	E	T	372
AAA	TAC	AAA	GAG	TTG	AAC	AAA	GAA	ACT	TCA	CGC	TGG	ACT	ACT	TAT	AGG	GGC	CCT	GAG	ACC	1147
N	P	R	P	G	S	C	S	V	G	P	S	S	D	K	A	L	T	F	M	392
AAC	CCC	CGG	CCA	GGC	AGT	TGC	TCA	GTG	GGC	CCC	TCC	TCT	GAT	AAG	GCC	CTG	ACC	TTC	ATG	1207
K	D	H	F	L	M	D	E	Q	V	V	G	T	P	L	L	V	K	S	G	412
AAG	GAC	CAT	TTC	CTG	ATG	GAT	GAG	CAA	GTG	GTG	GGG	ACG	CCC	CTG	CTG	GTG	AAA	TCT	GGC	1267
V	E	Y	T	R	L	A	V	E	T	A	Q	G	L	D	G	H	S	H	L	432
GTG	GAG	TAT	ACA	CGG	CTT	GCA	GTG	GAG	ACA	GCC	CAG	GGC	CTT	GAT	GGG	CAC	AGC	CAT	CTT	1327
V	M	Y	L	G	T	T	T	G	S	L	H	K	A	V	V	S	G	D	S	452
GTC	ATG	TAC	CTG	GGA	ACC	ACC	ACA	GGG	TCG	CTC	CAC	AAG	GCT	GTG	GTA	AGT	GGG	GAC	AGC	1387
S	A	H	L	V	E	E	I	Q	L	F	P	D	P	E	P	V	R	N	L	472
AGT	GCT	CAT	CTG	GTG	GAA	GAG	ATT	CAG	CTG	TTC	CCT	GAC	CCT	GAA	CCT	GTT	CGC	AAC	CTG	1447
Q	L	A	P	T	Q	G	A	V	F	V	G	F	S	G	G	V	W	R	V	492
CAG	CTG	GCC	CCC	ACC	CAG	GGT	GCA	GTG	TTT	GTA	GGC	TTC	TCA	GGA	GGT	GTC	TGG	AGG	GTG	1507
P	R	A	N	C	S	V	Y	E	S	C	V	D	C	V	L	A	R	D	P	512
CCC	CGA	GCC	AAC	TGT	AGT	GTC	TAT	GAG	AGC	TGT	GTG	GAC	TGT	GTC	CTT	GCC	CGG	GAC	CCC	1567
H	C	A	W	D	P	E	S	R	T	C	C	L	L	S	A	P	N	L	N	532
CAC	TGT	GCC	TGG	GAC	CCT	GAG	TCC	CGA	ACC	TGT	TGC	CTC	CTG	TCT	GCC	CCC	AAC	CTG	AAC	1627

Fig. 27C

# LOCUS: GEF360

321/361

S	W	K	Q	D	M	E	R	G	N	P	E	W	A	C	A	S	G	P	M	552
TCC	TGG	AAG	CAG	GAC	ATG	GAG	CGG	GGG	AAC	CCA	GAG	TGG	GCA	TGT	GCC	AGT	GGC	CCC	ATG	1687
S	R	S	L	R	P	Q	S	R	P	Q	I	I	K	E	V	L	A	V	P	572
AGC	AGG	AGC	CTT	CGG	CCT	CAG	AGC	CGC	CCG	CAA	ATC	ATT	AAA	GAA	GTC	CTG	GCT	GTC	CCC	1747
N	S	I	L	E	L	P	C	P	H	L	S	A	L	A	S	Y	Y	W	S	592
AAC	TCC	ATC	CTG	GAG	CTC	CCC	TGC	CCC	CAC	CTG	TCA	GCC	TTG	GCC	TCT	TAT	TAT	TGG	AGT	1807
H	G	P	A	A	V	P	E	A	S	S	T	V	Y	N	G	S	L	L	L	612
CAT	GGC	CCA	GCA	GCA	GTC	CCA	GAA	GCC	TCT	TCC	ACT	GTC	TAC	AAT	GGC	TCC	CTC	TTG	CTG	1867
I	V	Q	D	G	V	G	G	L	Y	Q	C	W	A	T	E	N	G	F	S	632
ATA	GTG	CAG	GAT	GGA	GTT	GGG	GGT	CTC	TAC	CAG	TGC	TGG	GCA	ACT	GAG	AAT	GGC	TTT	TCA	1927
Y	P	V	I	S	Y	W	V	D	S	Q	D	Q	T	L	A	L	D	P	E	652
TAC	CCT	GTG	ATC	TCC	TAC	TGG	GTG	GAC	AGC	CAG	GAC	CAG	ACC	CTG	GCC	CTG	GAT	CCT	GAA	1987
L	A	G	I	P	R	E	H	V	K	V	P	L	T	R	V	S	G	G	A	672
CTG	GCA	GGC	ATC	CCC	CGG	GAG	CAT	GTG	AAG	GTC	CCG	TTG	ACC	AGG	GTC	AGT	GGT	GGG	GCC	2047
A	L	A	A	Q	Q	S	Y	W	P	H	F	V	T	V	T	V	L	F	A	692
GCC	CTG	GCT	GCC	CAG	CAG	TCC	TAC	TGG	CCC	CAC	TTT	GTC	ACT	GTC	ACT	GTC	CTC	TTT	GCC	2107
L	V	L	S	G	A	L	I	I	L	V	A	S	P	L	R	A	L	R	A	712
TTA	GTG	CTT	TCA	GGA	GCC	CTC	ATC	ATC	CTC	GTG	GCC	TCC	CCA	TTG	AGA	GCA	CTC	CGG	GCT	2167

Fig. 27D

R	G	K	V	Q	G	C	E	T	L	R	P	G	E	K	A	P	L	S	R	732
CGG	GGC	AAG	GTT	CAG	GGC	TGT	GAG	ACC	CTG	CGC	CCT	GGG	GAG	AAG	GCC	CCG	TTA	AGC	AGA	2227
E	Q	H	L	Q	S	P	K	E	C	R	T	S	A	S	D	V	D	A	D	752
GAG	CAA	CAC	CTC	CAG	TCT	CCC	AAG	GAA	TGC	AGG	ACC	TCT	GCC	AGT	GAT	GTG	GAC	GCT	GAC	2287
N	N	C	L	G	T	E	V	A	*											762
AAC	AAC	TGC	CTA	GGC	ACT	GAG	GTA	GCT	TAA											2317
ACT	CTA	GGC	ACAGG	CGG	GCT	GCG	GTG	CAG	GCACCT	GGCCAT	GTCT	GGCT	GGCGGCC	CCCAAG	CACAG	CCCT	GACT	AGGA		2396
TG	ACAG	CAC	ACAAA	AGAC	CACTT	TCT	CCCT	GAG	AGAGCTT	CTGCT	ACTCT	GCAT	CTGCA	TCACT	GATG	ACACT	CAGC	AGGG		2475
TG	ATG	CAC	AGC	AGT	CTG	CCCT	TAT	GGG	ACTCCCT	TCT	ACCA	AGCAC	ATG	AGCT	CTCT	AAC	AGGT	GGGG	CTAC	2554
CC	AGAC	CTG	CTC	TAC	ACT	GAT	ATT	GA	GAACCT	GGAG	AGAT	CCTT	CAG	TTCT	GGCC	ATTC	CCAGG	ACCC	TCC	2633
CAC	AGT	GTTC	CA	AGAT	CC	TAAAA	AACT	CGCT	GTCC	AGG	ACCC	TAT	GGT	AAT	GAAC	ACCA	CACT	CCCT	TCT	2712
AT	ATG	CTA	ACAT	GCC	ACT	CC	TGG	AACT	CCACT	CTG	AA	CGT	CGCG	TT	TGG	ACAC	CACT	CCCT	TCT	2791
TG	CAG	GGAT	CTG	CTC	CTG	CTT	CCCT	TAC	CAGT	CGT	GC	ACCG	CTG	ACT	CCC	AGGA	GTCT	TT	CCT	2870
AC	CTT	CTT	CTT	CTG	CTT	CAG	TTGG	GCAG	ACT	CTG	AT	CCCT	TCT	GCC	CTG	CAGA	ATG	GC	AGG	2949
TC	ACT	CCCTT	TAC	CCCTAG	CTG	ACCC	CTT	CAC	CTCT	CCCC	CTCC	CTT	TT	CCCT	TTT	TGG	ATT	CAG	AAAA	3028
AG	AGACT	GTTT	TAT	TTTTT	TAT	TAAAA	ATATA	AGG	CTTAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	3104

Fig. 27E

Hum.	10	20	30	40	50	60	70
	MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLS						
	.....	.....	.....	.....	.....	.....	.....
Mur.	10	20	30	40	50	60	70
	MALPSLGQDSWSLLRVFFFLQLLPSLPPASGTGGQGPMPRVKYHAGDGHRALESFFQKGLRDFDTLLS						
	.....	.....	.....	.....	.....	.....	.....
Hum.	80	90	100	110	120	130	140
	GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY						
	.....	.....	.....	.....	.....	.....	.....
Mur.	80	90	100	110	120	130	140
	DDGNTLYVGARETVLALNIQNPGIPRLKNMIPWASERKKTECAFKKKSNETQCFNFIRVLVSYNATHLY						
	.....	.....	.....	.....	.....	.....	.....
Hum.	150	160	170	180	190	200	210
	TCGTFAFSPACTFIELQDSYLLPISEDKVMEKGQSPFPAKHHTAVLVDGMLYSGTMNNFLGSEPILMR						
	.....	.....	.....	.....	.....	.....	.....
Mur.	150	160	170	180	190	200	210
	ACGTFAFSPACTFIELQDSLLLPILIDKVMGKGQSPLTLFTSTQAVLVDGMLYSGTMNNFLGSEPILMR						
	.....	.....	.....	.....	.....	.....	.....
Hum.	220	230	240	250	260	270	280
	TLGSQPVLTNDNFLRWLHHDASFVAaipSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQ						
	.....	.....	.....	.....	.....	.....	.....
Mur.	220	230	240	250	260	270	280
	TLGSHPVLTNDI FLRWLHADASFVAaipSTQVVYFFFEETASEFDFFEEELYISRVAQVCKNDVGGEKLLQ						
	.....	.....	.....	.....	.....	.....	.....

Fig. 27F

Hum.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
	.....	.....	.....	.....	.....	.....	.....
Mur.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
	.....	.....	.....	.....	.....	.....	.....
Hum.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLKSGVEYTRLAV						
	.....	.....	.....	.....	.....	.....	.....
Mur.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFLMDEHVVGTPPLLKSGVEYTRLAV						
	.....	.....	.....	.....	.....	.....	.....
Hum.	430	440	450	460	470	480	490
	ETAQGLDGHSHLVMYLGTTTGLHKAUVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGA VFGFSGGVW						
	.....	.....	.....	.....	.....	.....	.....
Mur.	430	440	450	460	470	480	490
	ESARGLDGSSHVMYLGTTSTGPLHKA VVPQDSSAYLVEEIQ LSPDSEPVNRNLQ LAPAQGA VFAFGSGGIW						
	.....	.....	.....	.....	.....	.....	.....
Hum.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCVLARDPHCAWD PESRTCCLLSAPNLNSWKQDMERGNPEWACASGPM SRSRLRPQS						
	.....	.....	.....	.....	.....	.....	.....
Mur.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCVLARDPHCAWD PESRLCSLLSGST-KPWKQDMERGNPEWVCTRGPMARSRRRQS						
	.....	.....	.....	.....	.....	.....	.....

Fig. 27G



# TOP SECRET

Hum.	570	580	590	600	610	620	630
	RPQIIKEVLAVPNSILELPCPHLSALASYW	SHGPAAVPEASSTVYNGSLLLLIVQDGVGGLYQCWATENG					
Mur.	560	570	580	590	600	610	620
	PPQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKISEASATVYNGSLLLLLPQDGVGGLYQCVATENG						
Hum.	640	650	660	670	680	690	700
	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGAALAAQSYWPHFVTVTLFALVLSGALI						
Mur.	630	640	650	660	670	680	690
	YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVL						
Hum.	710	720	730	740	750	760	
	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA						
Mur.	700	710	720	730	740	750	760
	LLASPLGALRARGKVQCGMLPPREKAPLSRDQHLQPSKDHRTSASDVDADNNHLGAEVA						

Fig. 27H

**Fig. 27I**

Hum. ATGGAATACTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCC  
::: ::  
Mur. ATGGCAACACTCTCTATGTGGGGCTCGAGAGACCGTCCTGGCCTTGAATATCCAGAACCAGGAATCCC  
280 290 300 310 320 330 340

Hum. CAGGCTAAAGAACAATGATACCGTGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG  
:::  
Mur. AAGGCTAAAGAACAATGATACCGTGCCAGCCAGTGAGAGAAAAAAGACCGAATGTGCCTTTAAGAAGAAG  
350 360 370 380 390 400 410

Hum. AGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTCTTACAATGTACCCATCTCTACACCT  
:  
Mur. AGCAATGAGACACAGTGTTTCAACTTCATTGAGTCCCTGGTCTCTTACAATGCTACTCACCTCTATGCCT  
420 430 440 450 460 470 480

Hum. GCGGCACCTTCGCCCTTCAGCCCTGCTTGTAACCTTCATTGAACCTCAAGATTCCCTACCTGTTGCCCATCTC  
:  
Mur. GTGGACCTTTGCCCTTCAGCCCTGCCTGTACCTTCATTGAACCTCCAAGATTCCCTCCTGTTGCCCATCTT  
490 500 510 520 530 540 550

**Fig. 27J**

	530	540	550	560	570	580	590
Hum.	GGAGGACAAGGTCA	TGGAGGAAAGGCCA	AAGCCCTTTGACCCCGCTC	ACAAGCATACG-GCTGTCTT			
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
Mur.	GATAGACAAGGTCA	TGACGGGAAGGCCA	AAGCCC-TTTGACCCTG	TTCAAGCACACAAGCTGTCTT			
	560	570	580	590	600	610	620
Hum.	GGTGATGGGATGCT	CTATTCTGGTACTAT	GAACAACCTCCTGGCAGTAGCCCATCCTGATGCGCACACA				
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
Mur.	GGTCGATGGGATGC	TTTATTCGGGCACCAT	GAACAACCTTCTTGGCAGCGAGCCCATCCTGATGCGGACACA				
	630	640	650	660	670	680	690
Hum.	CTGGGATCCCAGCC	TGTCCTCAAGACCGACA	AACTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGG				
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
Mur.	CTGGGATCCCCATC	CCTGTTCTCAAGACTGACAT	CTTCTTACGCTGGCTGCACGCGGATGCCTCCTTCGTGG				
	700	710	720	730	740	750	760
Hum.	740	750	760	770	780	790	800
	CAGCCATCCCCTTC	GACCCAGGTCGTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA					
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
Mur.	CAGCCATTCCATCC	ACCCAGGTCGTCTATTCTTCTTGGAGAGACAGCCAGCGAGTTTGACTTCTTTGA					
	770	780	790	800	810	820	830

**Fig. 27K**

**Fig. 27L**

1090	1100	1110	1120	1130	1140	1150
Hum.	GGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGCCCTGAGACCAACCCCC					
	::					
Mur.	GGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGCTCAGAGGTCAGCCCCGA					
1120	1130	1140	1150	1160	1170	1180
1160	1170	1180	1190	1200	1210	1220
Hum.	GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTTGAT					
	::					
Mur.	GGCCAGGCAGTTGCTCCATGGGCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTTCTGAT					
1190	1200	1210	1220	1230	1240	1250
1230	1240	1250	1260	1270	1280	1290
Hum.	GGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAG					
	::					
Mur.	GGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGTGTGGAG					
1260	1270	1280	1290	1300	1310	1320
1300	1310	1320	1330	1340	1350	1360
Hum.	ACAGCCCAGGGCCTTGATGGGCACAGCCCATCTTGTCATGTACCTGGGAACCAACACAGGGTCGCTCCACA					
	::					
Mur.	TCAGCTCGGGCCTTGATGGGAGCAGCCATGTGGTCAATGTGGTACCTCCACGGGTCCCTGCACA					
1330	1340	1350	1360	1370	1380	1390

Fig. 27M

	1370	1380	1390	1400	1410	1420	1430
Hum.	AGGCTGTGGTAAGTGGGGACAGCAGTGTCTCATCTGGTGGAGAGATTTCAGCTGTTCCCTGACCCCTGAACC						
	::::::::::	:	::::::::::	::::	::::::::::	::::::::::	::::::::::
Mur.	AGGCTGTGTGCCTCAGGACAGCAGTGTATCTCGTGGAGGAGATTTCAGCTGAGCCCTGACTCTGAGCC						
	1400	1410	1420	1430	1440	1450	1460
	1440	1450	1460	1470	1480	1490	1500
Hum.	TGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGTGTCTGGAGG						
	:::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	TGTTCGAAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGGCATCTGGAGA						
	1470	1480	1490	1500	1510	1520	1530
	1510	1520	1530	1540	1550	1560	1570
Hum.	GTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCTTGCCTGGACCCCTGCTGTG						
	:: :::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	GTTCCCAGGGCCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAGGGACCCCTCACTGTG						
	1540	1550	1560	1570	1580	1590	1600
	1580	1590	1600	1610	1620	1630	1640
Hum.	CCTGGGACCCCTGAGTCCCCGAACCTGTTGCCCTCCTGTCTGTGCCCCCAACCTGAACCTCCTGGAAGCAGGACAT						
	::::::::::	::::::::::	:: :::	::::::::::	:: :::	::::::::::	::::::::::
Mur.	CCTGGGACCCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAGCAGGACAT						
	1610	1620	1630	1640	1650	1660	1670

Fig. 27N

	1650	1660	1670	1680	1690	1700	1710
Hum.	GGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGC						
	1680	1690	1700	1710	1720	1730	1740
Mur.	GGAACGCGGCAACCCGAGTGGGTATGCACCCGTGGCCCCATGCCCAGGAGCCCCGGCGTCAGAGCCCC						
	1720	1730	1740	1750	1760	1770	1780
Hum.	CCGCAATCATTAAGAGTCCTGGCTGTCCCAACTCCATCCTGGAGTCCCTGCCCCACCTGTCTAG						
	1750	1760	1770	1780	1790	1800	1810
Mur.	CCTCAACTAATTAAGAGTCCTGACAGTCCCCCAACTCCATCCTGGAGCTGCGTGCCCCCACCTGTCTAG						
	1790	1800	1810	1820	1830	1840	1850
Hum.	CCTTGGCCTCTTATTATGGAGTCATGGCCAGCAGCAGTCCCAGAGCCTCTTCCACTGTCTACAATGG						
	1820	1830	1840	1850	1860	1870	1880
Mur.	CACTGGCCTCTTACCACTGGAGTCATGGCCGAGCCAAATCTCAGAGCCTCTGTACTCCGTCTACAATGG						
	1860	1870	1880	1890	1900	1910	1920
Hum.	CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAAATGGCTTT						
	1890	1900	1910	1920	1930	1940	1950
Mur.	CTCCCTCTTGCTGCTGCCGAGGATGGTGTCTGGGGCCTCTACCAGTGTGTGGCGACTGAGAACGGCTAC						

Fig. 270



	1930	1940	1950	1960	1970	1980	1990
Hum.	TCATACCCCTGTGATCTCCTACTGGGTGGACAGCCAGGACACCCCTGGCCCTGGATCCTGAACTGGCAG						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	TCATACCCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCCCTGGCGCTGGACCCCTGAGCTGGCGG						
	1960	1970	1980	1990	2000	2010	2020
	2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCCGGAGCATGTGAAGTCCCGTTGACCAGGGTCAGTGGTGGGCGCCCTGGCTGCCACGCA						
	::::	::::	::::	::::	::::	::::	::::
Mur.	GCGTTCCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGGCGGAGCTTCCATGGCTGCCACGCG						
	2030	2040	2050	2060	2070	2080	2090
	2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCCTACTGGCCCCACATTGTCACTGTCACTGTCTCTTTGCCCTTAGTGCTTTCAGGAGCCCTCATCATC						
	::::::::::	::::	::::	::::	::::	::::	::::
Mur.	GTCCCTACTGGCCCCCATTTTCTCATCGTTACCGTCCCTGCGCCATCGTGCTCCTGGGAGTGCTCACTCTC						
	2100	2110	2120	2130	2140	2150	2160
	2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCCCTGCGCCCTG						
	:::	::	::::	::::	::::	::::	::::
Mur.	CTCCTCGCTTCCCCACTGGGGCGCTGCGGGCTCGGGGTAAAGTTCAAGGCTGTGGGATGCTGCCCCCA						
	2170	2180	2190	2200	2210	2220	2230

Fig. 27P

```

2210      2220      2230      2240      2250      2260      2270
Hum.  GGGAGAAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGGAAAGGCTCCACTGAGCAGGAGCACACCTCCAGCCCTCCAAGGACCACACAGGACCTCTGCCAGTGA
2240      2250      2260      2270      2280      2290      2300

2280      2290      2300      2310      2320      2330      2340
Hum.  TGTGGACGCTGACAACTGCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGG-CCGGGGCTG--C
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CGTAGATCCCGACAAACCATCTGGGCGCGCGAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC
2310      2320      2330      2340      2350      2360      2370

2350      2360      2370      2380      2390      2400      2410
Hum.  GGTGCAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AGAGCAAAGCCACTGGCCTTGTGGCTATGC-----CAGGCACAG-----TGCCACTCT--
2380      2390      2400      2410      2420

2420      2430      2440      2450      2460      2470      2480
Hum.  AGACCACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  -GACCA-----GGGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTCAC-CTACAG-----C
2430      2440      2450      2460

```

Fig. 27Q

	2490	2500	2510	2520	2530	2540	2550
Hum.	ACAGCAGTCTG-CCTCCCTATGGGACTCCCCTTCTACCAAGCACATGAGCTCTCTAAACAGGGTGGGGGCT						
	:: :::: : :::::::::::::::::::: :::::						:::::
Mur.	ACC-CAGTAGGTCTCCCTGTGGGACTCTCTTGTC-AAGCACATT-----GGGCT						
	2470	2480	2490	2500	2510		
	2560	2570	2580	2590	2600	2610	
Hum.	ACCCCCAGACCTGCTCTACACTGATA-TTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCAATCCAG						
	. : :::: :: : . :::: : . :::::::::::::: :::: :::: :::: :::: ::::						
Mur.	GTCGCCATACCTGTACTTGTGCTGTGACAGGAAGAGCCAGAC-AGGTTTCTTTGATTTTGATTGACCCCAA						
	2520	2530	2540	2550	2560	2570	2580
	2620	2630	2640	2650	2660	2670	2680
Hum.	GGACCCCT-CCAGAAACACA-GTGTTTCAAGAGATCCTAAAAAACCTGCCTGTCCCAGGACCCATATGTA						
	: ::::: ::::::::::: : :::: : :::::::::::::: :::: :::: :::: :::: ::::						
Mur.	GAGCCCTGCCTGTAAACAAACGTGCTCCAGGAGA-CCATGAAAGGTGTGGCTGTCT-GGGATTCTGTGGTG						
	2590	2600	2610	2620	2630	2640	2650
	2690	2700	2710	2720	2730	2740	2750
Hum.	ATGAACACCAAACATCTAAACAATCATATGCTAA-CATGC---CAC--TCCTGGAAACT-CCACTCTGAA						
	: :::: : ::::::::::: ::::::::::: . . ::::: : :::: : :::: :::: :::: ::::						
Mur.	ACAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCTCTGCAAACTCCATCCTGAACGCTGTCACTCTAGA						
	2660	2670	2680	2690	2700	2710	2720

**Fig. 27R**

Hum.	2760	2770	2780	2790	2800	2810
	---GCTGCCGCTTTGGACACCAACACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC					
	:::: ::::::::::::::: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::					
Mur.	AGCAGCTGCTGCTTTGAACACCAAGCCACCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT					
	2730	2740	2750	2760	2770	2780
	2790					
Hum.	2820	2830	2840	2850	2860	2870
	2880					
	TTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTTC					
	:::: ::::::::::::::: :: :::::::::: ::::::::::::::: ::::::::::::::: ::::::::::::::: ::					
Mur.	TTCCTTTACCAGTCGGGCCATACTGTTT--GGGAAGTCATCTCTGAAGTCTAACCACTTCCCTTCTTGG					
	2800	2810	2820	2830	2840	2850
Hum.	2890	2900	2910	2920	2930	2940
	2950					
	TTCAGTTGGGGCAGACTCTGATCCCT--TCTGCCCTGGCAGAATGCGAGGGGTAATCTGAGCCTTCTTC					
	:::: ::::::::::::::: :: :: ::::::::::::::: ::::::::::::::: ::::::::::::::: ::					
Mur.	TTCAGTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAGAAATGGGGGCATAATCTGAGCCTTGTTC					
	2860	2870	2880	2890	2900	2910
	2920					
Hum.	2960	2970	2980	2990	3000	3010
	ACTCCTTTTACCC---TAGCTGACCCCTTCACCTCTCCC--CCTCCCTTTTCCCTTGTTTTGGGATTACAGA					
	:::: :: ::::::::::::::: :: :::::::::: :: :::::::::: :: :::::::::: :: :::::::::: ::					
Mur.	---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTCCCTTCCCTCC---TCCCTTGTTTTGGGATTACAGA					
	2930	2940	2950	2960	2970	2980
	2990					

**Fig. 27S**



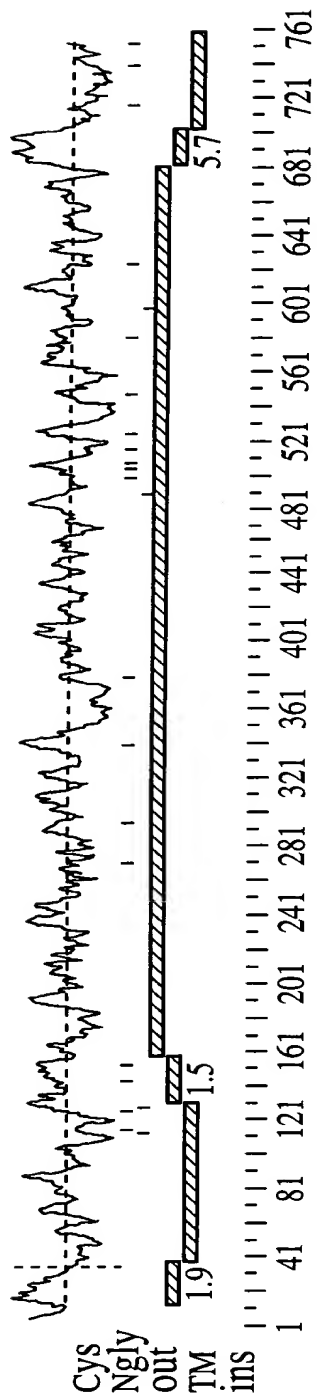


Fig. 27U

GTCGACCCACGCGTCCGACGCTTTGGACACTTCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGCAACTAAAGGA	79
TCAAGAAAGGCCAGCACAGCAGAAAGATCAGCTGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC	150
M C T K T I	
P V L W G C F L L W N L Y V S S S Q T I	6
CCA GTC CTC TGG GGA TGT TTC CTC CTG TGG AAT CTC TAT GTC TCA TCC TCT CAG ACC ATT	26
Y P G I K A R I T Q R A L D Y G V Q A G	46
TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GGT CAA GCT GGA	270
M K M I E Q M L L K E K K L P D L S G S E	66
ATG AAG ATG ATT GAG CAA ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG	330
S L E F L K V D Y V N Y N F S N I K I S	86
TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT	390
A F S F P N T S L A F V P G V G I K A L	106
GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA	450
T N H G T A N I S T D W G F E S P L F V	126
ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT	510
L Y N S F A E P M E K P I L K N L N E M	146
CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG	570

339/361

Fig. 28A

# LOCUS DEFB60

L	C	P	I	I	A	S	E	V	K	A	L	N	A	N	L	S	T	L	E	166
CTC	TGT	CCC	ATT	ATT	GCA	AGT	GAA	GTC	AAA	GCG	CTA	AAT	GCC	AAC	CTC	AGC	ACA	CTG	GAG	630
V	L	T	K	I	D	N	Y	T	L	L	D	Y	S	L	I	S	S	P	E	186
GTT	TTA	ACC	AAG	ATT	GAC	AAC	TAC	ACT	CTG	CTG	GAT	TAC	TCC	CTA	ATC	AGT	TCT	CCA	GAA	690
I	T	E	N	Y	L	D	L	N	L	K	G	V	F	Y	P	L	E	N	L	206
ATT	ACT	GAG	AAC	TAC	CTT	GAC	CTG	AAC	TTG	AAG	GGT	GTA	TTC	TAC	CCA	CTG	GAA	AAC	CTC	750
T	D	P	P	F	S	P	V	P	F	V	L	P	E	R	S	N	S	M	L	226
ACC	GAC	CCC	CCC	TTC	TCA	CCA	GTT	CCT	TTT	GTG	CTC	CCA	GAA	CGC	AGC	AAC	TCC	ATG	CTC	810
Y	I	G	I	A	E	Y	F	F	K	S	A	S	F	A	H	F	T	A	G	246
TAC	ATT	GGA	ATC	GCC	GAG	TAT	TTC	TTT	AAA	TCT	GCG	TCC	TTT	GCT	CAT	TTC	ACA	GCT	GGG	870
V	F	N	L	T	L	S	T	E	E	I	S	N	H	F	V	Q	N	S	Q	266
GTT	TTC	AAT	CTC	ACT	CTC	TCC	ACC	GAA	GAG	ATT	TCC	AAC	CAT	TTT	GTT	CAA	AAC	TCT	CAA	930
G	L	G	N	V	L	S	R	I	A	E	I	Y	I	L	S	Q	P	F	M	286
GGC	CTT	GGC	AAC	GTG	CTC	TCC	CGG	ATT	GCA	GAG	ATC	TAC	ATC	TTG	TCC	CAG	CCC	TTC	ATG	990
V	R	I	M	A	T	E	P	P	I	I	N	L	Q	P	G	N	F	T	L	306
GTG	AGG	ATC	ATG	GCC	ACA	GAG	CCT	CCC	ATA	ATC	AAT	CTA	CAA	CCA	GGC	AAT	TTC	ACC	CTG	1050
D	I	P	A	S	I	M	M	L	T	Q	P	K	N	S	T	V	E	T	I	326
GAC	ATC	CCT	GCC	TCC	ATC	ATG	ATG	CTC	ACC	CAA	CCC	AAG	AAC	TCC	ACA	GTT	GAA	ACC	ATC	1110

340/361

Fig. 28B



V	S	M	D	F	V	A	S	T	S	V	G	L	V	I	L	G	Q	R	L	346
GTT	TCC	ATG	GAC	TTC	GTT	GCT	AGT	ACC	AGT	GTT	GGC	CTG	GTT	ATT	TTG	GGA	CAA	AGA	CTG	1170
V	C	S	L	S	L	N	R	F	R	L	A	L	P	E	S	N	R	S	N	366
GTC	TGC	TCC	TTG	TCT	CTG	AAC	AGA	TTC	CGC	CTT	GCT	TTG	CCA	GAG	TCC	AAT	CGC	AGC	AAC	1230
I	E	V	L	R	F	E	N	I	L	S	S	I	L	H	F	G	V	L	P	386
ATT	GAG	GTC	TTG	AGG	TTT	GAA	AAT	ATT	CTA	TCG	TCC	ATT	CTT	CAC	TTT	GGA	GTC	CTC	CCA	1290
L	A	N	A	K	L	Q	Q	G	F	P	L	P	N	P	H	K	F	L	F	406
CTG	GCC	AAT	GCA	AAA	TTG	CAG	CAA	GGA	TTT	CCT	CTG	CCC	AAT	CCA	CAC	AAA	TTC	TTA	TTC	1350
V	N	S	D	I	E	V	L	E	G	F	L	L	I	S	T	D	L	K	Y	426
GTC	AAT	TCA	GAT	ATT	GAA	GTT	CTT	GAG	GGT	TTC	CTT	TTG	ATT	TCC	ACC	GAC	CTG	AAG	TAT	1410
E	T	S	S	K	Q	Q	P	S	F	H	V	W	E	G	L	N	L	I	S	446
GAA	ACA	TCC	TCA	AAG	CAG	CAG	CCA	AGT	TTC	CAC	GTA	TGG	GAA	GGT	CTG	AAC	CTG	ATA	AGC	1470
R	Q	W	R	G	K	S	A	P	*											456
AGA	CAG	TGG	AGG	GGG	AAG	TCA	GCC	CCT	TGA											1500
TTGCCGGTTT	GCAATT	CACCC	CAGGAAGT	AAATGGT	CCCTTAAT	CCTACA	ACTACTGT	AAACCC	CAGAAAGG	AAAGACAGT	1579									
ACACACTGGAAT	TGTAAAGCCCTT	GTGAATTG	CTTAGGC	AGAAAGTTT	CTTTCTTA	AGCCTT	CAGGAACCC	CAGAAATAA	1658											
GGCAGACTCTG	TAAAGGGATAA	TAGAGGTGT	CTGAATGT	GAGTGATG	CATGCTG	CTGTGTT	TATGTTG	1737												
TTTGTGTTT	GGGCAAGAA	GATCTTAG	GACAAGAGCT	AGGATGTACTT	CTGACC	AGGTGGT	AAGCAACTCTAAG	1816												

Fig. 28C

342/361

342/361

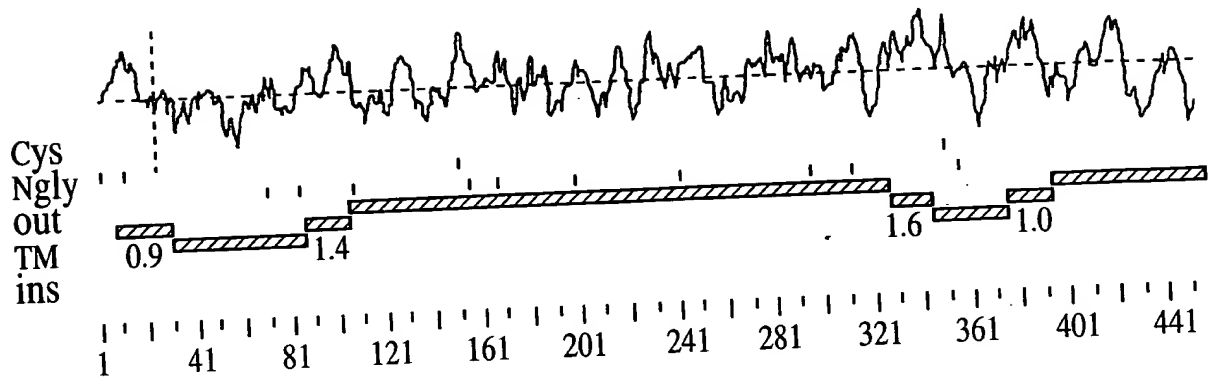


Fig. 28E

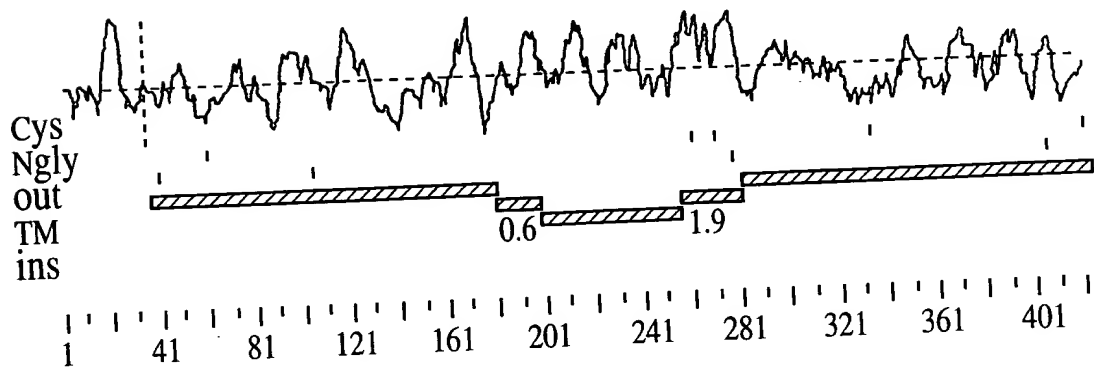


Fig. 29F

FOOT-026960

# Figure 28F

```

10      20      30      40      50      60
286 MCTKT-IPVLWGCFL-LWNLVSSSQTIPGIKARITQRALDYGVDAGMKMIEQMLKEKKLPDLSGSESL
:      :      :      :      :      :      :      :      :      :      :      :
BPI MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNFNFSNIKISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPM--
:      :      :      :      :      :      :      :      :      :      :      :
BPI KIKHLKGHYFSYMDIREFQLPSSQISMVNVGLKFSISNANIKISGKWKAKQRFKMKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----140     150
:      :      :      :      :      :      :      :      :      :      :      :
BPI SISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDNLKGVFYPLENLTDPFSPVPFVLPERSN
:      :      :      :      :      :      :      :      :      :      :      :
BPI VSSKLQPYFQTLPMVKIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHNPPFPFAPVMEFFPAHD
210     220     230     240     250     260     270

```

Fig. 28F

**Fig. 28G**

	10	20	30	40	50	60
286	MCTKTIPVLWGCFLWNLYVSSSQTI--YPGIKARITQRALDYGVAQGMKMIQMLKEKKLPDLGSESL					
	: . . . .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .
RENP	MGALARAL--PSILLALLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL					
	10	20	30	40	50	60
70	80	90	100	110	120	130
286	EFLKVDYVNYNFSNIKISAFSEFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--					
	. : .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .
RENP	RIPHVGRGRYEFHSLNIHEFQLPSSQISMVPNVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM					
	70	80	90	100	110	120
						130
286	-----KPI-----					
					140	150
					---LKN-INEMLCPIIASE	
RENP	SISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVKVGLIQLFHKKIESALRNKMNSQVCEKVTNS					
	140	150	160	170	180	190
						200
286	160	170	180	190	200	210
						220
286	VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDLNLKGVFYPLENLTDPFPSPVFLPERSN					
	: . . . .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .	: : : : . . . . .
RENP	VSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAH					
	210	220	230	240	250	260
						270

Fig. 28H

**Fig. 28I**

GTCGACCCACGCGTCCGGGAATTGCAGCAGGAAATAATGTGAAGAGTTTTTAAACCCACAAAATCTTCTTACTTTAGA	79
M L E T L S R Q	
ATTAGTTGTTACATTGCAGGAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG	8 149
W I V S H R M E M W L L I L V A Y M F Q	28
TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG	209
R N V N S V H M P T K A V D P E A F M N	48
AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT	269
I S E I I Q H Q G Y P C E E Y E V A T E	68
ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA	329
D G Y I L S V N R I P R G L V Q P K K T	88
GAT GGG TAT ATC CTT TCT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA	389
G S R P V V L L Q H G L V G A S N W I	108
GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT	449
S N L P N N S L G F I L A D A G F D V W	128
TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG	509
M G N S R G N A W S R K H K T L S I D Q	148
ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA	569

Fig. 29A



D E F W A F S Y D GAT GAT GAG ATG M A R F D L P A V I 168  
GAT GAG TTC TGG GCT TTC AGT TAT GAT GAT GAG ATG GCT AGG TTT GAC CTT CCT GCA GTG ATA 629

N F I L Q K T G Q CAG GGC CAG GAA AAG ATC TAT TAT GTC GGC TAT TCA CAG GGC 188  
AAC TTT ATT TTG CAG AAA ACG GGC CAG GAA AAG ATC TAT TAT GTC GGC TAT TCA CAG GGC 689

T T M G F I A F S T M P E L A Q K I K M 208  
ACC ACC ATG GGC TTT ATT GCA TTT TCC ACC ATG CCA GAG CTG GCT CAG AAA ATC AAA ATG 749

Y F A L A P I A T V K H A K S P G T K F 228  
TAT TTT GCT TTA GCA CCC ATA GCC ACT GTT AAG CAT GCA AAA AGC CCC GGG ACC AAA TTT 809

L L L P D M M I K G L F G K K E F L Y Q 248  
TTG TTG CTG CCA GAT ATG ATG ATC AAG GGA TTG TTT GGC AAA AAA GAA TTT CTG TAT CAG 869

T R F L R Q L V I Y L C G Q V I L D Q I 268  
ACC AGA TTT CTC AGA CAA CTT GTT ATT TAC CTT TGT GGC CAG GTG ATT CTT GAT CAG ATT 929

C S N I M L L L G G F N T N M N M S R 288  
TGT AGT AAT ATC ATG TTA CTT CTG GGT GGA TTC AAC ACC AAC AAT ATG AAC ATG AGC CGA 989

A S V Y A A H T L A G T S V Q N I L H W 308  
GCA AGT GTA TAT GCT GCC CAC ACT CTT GCT GGA ACA TCT GTG CAA AAT ATT CTA CAC TGG 1049

S Q A V N S G E L R A F D W G S E T K N 328  
AGC CAG GCA GTG AAT TCT GGT GAA CTC CGG GCA TTT GAC TGG GGG AGT GAG ACC AAA AAT 1109

349/361

Fig. 29B

# Figure 29C

L	E	K	C	N	Q	P	T	P	V	R	Y	R	V	R	D	M	T	V	P	348
CTG	GAA	AAA	TGC	AAT	CAG	CCA	ACT	CCT	GTA	AGG	TAC	AGA	GTC	AGA	GAT	ATG	ACG	GTC	CCT	1169
T	A	M	W	T	G	G	Q	D	W	L	S	N	P	E	D	V	K	M	L	368
ACA	GCA	ATG	TGG	ACA	GGA	GGT	CAG	GAC	TGG	CTT	TCA	AAT	CCA	GAA	GAC	GTG	AAA	ATG	CTG	1229
L	S	E	V	T	N	L	I	Y	H	K	N	I	P	E	W	A	H	V	D	388
CTC	TCT	GAG	GTG	ACC	AAC	CTC	ATC	TAC	CAT	AAG	AAT	ATT	CCT	GAA	TGG	GCT	CAC	GTG	GAT	1289
F	I	W	G	L	D	A	P	H	R	M	Y	N	E	I	I	H	L	M	Q	408
TTC	ATC	TGG	GGT	TTG	GAT	GCT	CCT	CAC	CGT	ATG	TAC	AAT	GAA	ATC	ATC	CAT	CTG	ATG	CAG	1349
Q	E	E	T	N	L	S	Q	G	R	C	E	A	V	L	*					424
CAG	GAG	GAG	ACC	AAC	CTT	TCC	CAG	GGA	CGG	TGT	GAG	GCC	GTA	TTG	TGA					1397
AGCATCTGACACTGACGATCTTAGGACAAACCTCCTGAGGGATGGGGCTAGGACCCATGAAGGCAGAAATTACGGAGAGCA	1476																			
GAGACCTAGTATACATTTTTCAGATTCCCTGCACCTGGCACTAAATCCGACACTTACATTTTCTGTAAA	1555																			
TTAAAGTACTTATTAGGTAAATAGAGGTTTGTATGCTATTATATATCTACCATCTTGAAGGCTAGGTTTACCTGAT	1634																			
AGCCAGAAAATATCTAGACATTCTCTATATCATTCAGGTAAATCTCTTAAACACACCTATTGTTTTTCTATAAGCCAT	1713																			
ATTTTGGAGCACTAAAGTAAATGGCAAAATGGGACAGATATTGAGGCTCTGGAGCTGTGGATTATTGTTGACTTTGA	1792																			
CAAAATAAGCTAGACATTTTCACCTTGTGTCACAGACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA	1871																			
CAACAACAAAATCAGTGTACAGTATGGATGAAATCTATGTTAAGCATTCACAGAAATAAGGCCAAGTTTATAGTTGCA	1950																			
TCTCAGGGGAAGAAAATTTTATAGGATGTTTATGAGTTCTCCAATAAATGCATTCTGCATTACATAAAAAA	2029																			
AAAAAGGGCGGCCGC	2044																			

Fig. 29C

**Fig. 29D**

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	

```

280      290      300      310      320      330      340
294 NTNNMMSRASVYAAHTLAGTSVQNIILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVPT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP DSKNFNTSRLDVYLSHNPAGTSVQNMFHWTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVTAMNVPI
      270      280      290      300      310      320      330

      350      360      370      380      390      400      410
294 AMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
      . . . . . : : : : : : : : : : : : : : : : : : : : : : . . . .
HLP AVWNGGKDLLADPQDVGLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-----
      340      350      360      370      380      390

```

420

294 EAVL

HLP ---

**Fig. 29E**

[illegible][illegible]

**Fig. 29G**

```

280      290      300      310      320      330      340
294 FNTNNMNSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVP
::  ::::::::::::::::::::  ::::::::::::::::::::  ::::::::::::::::::::  ::::::::::::::::::::
LAL FNERNLNMSRVDVYTHSPAGTSVQNMLHWSQAVKFKQFAFDWGSSAKNYFHYNQSYPPITYNVKDMMLVP
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
::  ::::::::::::::::::::  ::::::::::::::::::::  ::::::::::::::::::::  ::::::::::::::::::::
LAL TAVWSGGHDWLADVVDVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKIINLMRKYQ-----
340      350      360      370      380      390

420
294 CEAVL

LAL -----

```

Fig. 29H

		M																S		2	
GTCGACCCACGGCTCCACGGCGAGGGCTCCCGGGGGCGAGCATTGCCCCCCCCCTGCACCACCTCACC AAG ATG GCT																				75	
T	L	G	H	T	F	P	F	Y	A	G	P	K	P	T	F	P	M	D	T	22	
ACT	TTG	GGA	CAC	ACA	TTC	CCC	TTC	TAT	GCT	GGC	CCC	AAG	CCA	ACC	TTC	CCG	ATG	GAC	ACC	135	
T	L	A	S	I	I	M	I	F	L	T	A	L	A	T	F	I	V	I	L	42	
ACT	TTG	GCC	AGC	ATC	ATC	ATG	ATC	TTT	CTG	ACT	GCA	CTG	GCC	ACG	TTC	ATC	GTC	ATC	CTG	195	
P	G	I	R	G	K	T	R	L	F	W	L	L	R	V	V	T	S	L	F	62	
CCT	GGC	ATT	CGG	GGA	AAG	ACG	AGG	CTG	TTC	TGG	CTG	CTT	CGG	GTG	GTG	ACC	AGC	TTA	TTC	255	
I	G	A	A	I	L	A	V	N	F	S	S	E	W	S	V	G	Q	V	S	82	
ATC	GGG	GCT	GCA	ATC	CTG	GCT	GTG	AAT	TTC	AGT	TCT	GAG	TGG	TCT	GTG	GGC	CAG	GTC	AGC	315	
T	N	T	S	Y	K	A	F	S	S	E	W	I	S	A	D	I	G	L	Q	102	
ACC	AAC	ACA	TCA	TAC	AAG	GCC	TTC	AGT	TCT	GAG	TGG	ATC	AGC	GCT	GAT	ATT	GGG	CTG	CAG	375	
V	G	L	G	G	V	N	I	T	L	T	G	T	P	V	Q	Q	L	N	E	122	
GTC	GGG	CTG	GGT	GGA	GTC	AAC	ATC	ACA	CTC	ACA	GGG	ACC	CCC	GTG	CAG	CAG	CTG	AAT	GAG	435	
T	I	N	Y	N	E	E	F	T	W	R	L	G	E	N	Y	A	E	E	C	142	
ACC	ATC	AAT	TAC	AAC	GAG	GAG	TTC	ACC	TGG	CGC	CTG	GGT	GAG	AAC	TAT	GCT	GAG	GAG	TGT	495	
A	K	A	L	E	K	G	L	P	D	P	V	L	Y	L	A	E	K	F	T	162	
GCA	AAG	GCT	CTG	GAG	AAG	GGG	CTG	CCA	GAC	CCT	GTG	TTG	TAC	CTA	GCT	GAG	AAG	TTC	ACT	555	

355/361

P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	GCG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

356/361

Fig. 30B



L	*	344
TTA	TAA	1101
CATTCCTCCCCGTGGAGGCCACCTGGACTTCCAGTCTGGCTCCAAACCTCAATTGGCGCCCCATAAAACCAGCAAACTG	1180	
CCCTCAGGGTGGCTGTTACCAAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT	1259	
AAAAACAAAACAAAACAAAAGCCCTAAGGACTGAAGAGATGCTGGGCTGTCCATAAAGCCCTGTTGCCATGATAAG	1338	
GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGCCTTCCGTGCTGCCCTTCCCTCTTCAAGATGCTATTCACCTGA	1417	
AACCTAACTTCAACCCCATAAACACAGCAGGTGGGGTTACATAATGATTCTCCATGTTTCCCTCTCATCCCTCGGCA	1496	
CCTCTTGTTCCTTTTTCCTGGGTTCCCTTTTGTTCCTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA	1575	
AGACAGCACTGGAAGAGGGGAAACCAAACTTCTCATCCTAGGTCTAACATTAACCAACTATGCCACATTCCTCTTGA	1654	
GCTTCAGTTCCCAAATTTGCTACATAAGATTGCAAGACTTGCCAAGAACTTGGGATTTATCTTCTATGCCCTTGCTGA	1733	
CACCTACCTTGGCCCTCAAACACACCCCTCACAAAGAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAACGCTATTCCT	1812	
TCCCACCCCACTCAGCTGGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGGTGACCTGCCCTCATCÄCTGCCACCTAA	1891	
CGTCCCCCTGGGTGTTCAGAAAGATGCTAGCTCTGGTAGGTCCCTCCGGCCTCACTAGAGGGCGCCCTATTACTC	1970	
TGGAGTCGACGCAGAGAAATCAGGTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCAGCGAAGCTCATGA	2049	
GGACGTGCGACCCCGCGGAGAGCCATGAAAAATTAATGGGAAAAACAGTTTTTAAAAAAGGGGCG	2128	
GCCGC	2133	

357/361

Fig. 30C

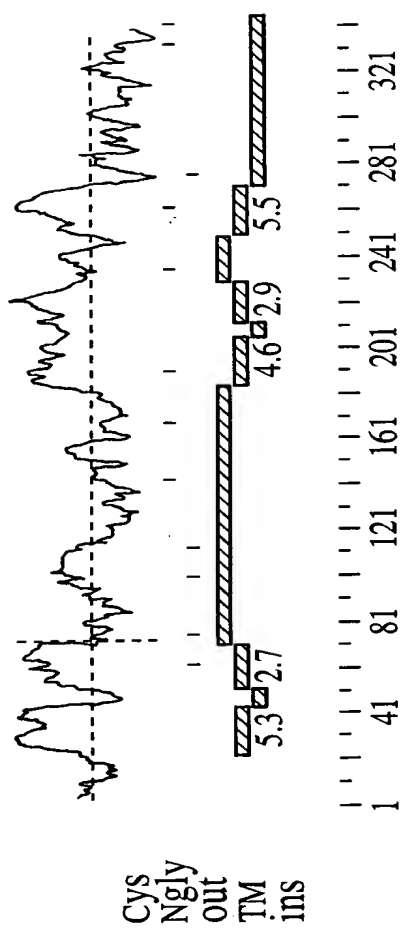


Fig. 30D

**Fig. 30E**

**Fig. 30F**

**Fig. 30G**